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OM nucleic - nucleic search, using sw model

Run on: March 21, 2005, 12:46:16 / Search time 5666.07 seconds
(without alignments)
10732.529 Million cell updates/sec

Title: US-10-643-627-3

Perfect score: 1255
Sequence: 1 CGCTCCAGGCGCCGGTGTGACA.....TTAAGACCTCATGAGT 1255

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb ba: *
2: gb ntg: *
3: gb ln: *
4: gb om: *
5: gb ov: *
6: gb pac: *
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8: gb pl: *
9: gb pr: *
10: gb ro: *
11: gb stb: *
12: gb sy: *
13: gb un: *
14: gb vi: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1255	100.0	1255	6	AR012638	AR012638 Sequence
2	1255	100.0	1255	6	AR171258	AR171258 Sequence
3	1255	100.0	1255	6	142455	142455 Sequence 3
4	1255	100.0	1255	6	187849	187849 Sequence 3
5	1247	99.4	18351	9	AF400075	AF400075 Homo sapi
6	1247	99.4	107278	9	AC114962	AC114962 Homo sapi
7	1247	99.4	184536	2	AC068682	AC068682 Homo sapi
8	1243.8	99.1	52358	9	AC010621	AC010621 Homo sapi
9	1211	96.5	1289	9	HSPAR2B	Z49994 H. sapiens p
10	1117	89.0	1451	6	CQ726252	BC012453 Homo sapi
11	1117	89.0	2813	9	BC018130	BC018130 Homo sapi
12	1115.4	88.9	2876	9	AY336105	AY336105 Homo sapi
13	1113.8	88.7	1451	6	CQ870621	CQ870621 Sequence
14	1113.8	88.7	1451	6	CQ876755	CQ876755 Sequence
15	1113.8	88.7	1451	6	AX549014	AX549014 Sequence
16	1113.8	88.7	1451	6	HSU34038	U34038 Human prote
17	1112	88.6	1194	9	BT009856	BT009856 Homo sapi
18	1105.8	88.1	1414	6	AR012640	AR012640 Sequence

20	1105.8	88.1	1414	6	AR171260	AR171260 Sequence
21	1105.8	88.1	1414	6	187851	187851 Sequence 62
22	1105.4	89.1	1124	9	HSU36753	U36753 Human prote
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24	1024.4	81.6	1026	6	CQ760413	CQ760413 Sequence
25	961.4	76.6	963	6	CQ760414	CQ760414 Sequence
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28	844.2	67.3	1475	6	AR012637	AR012637 Sequence
29	844.2	67.3	1475	6	AR171257	AR171257 Sequence
30	844.2	67.3	1475	6	142454	142454 Sequence 1
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35	817.4	65.1	2732	6	AR012639	AR012639 Sequence
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40	790.2	63.0	1428	10	RNU61373	U61373 Rattus norv
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43	570.4	45.5	91325	2	AC139936	AC139936 Mus muscu
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45	341.8	27.2	194749	2	BX842690	BX842690 Danio rer

ALIGNMENTS

RESULT 1
AR012638
LOCUS AR012638 Sequence 3 from patent US 5763575.
DEFINITION AR012638
ACCESSION AR012638
VERSION AR012638.1 GI:3970628
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1255)
AUTHORS Sundelin, J. and Scarborough, R.M.
TITLE Agonist and antagonist peptides of the C140 receptor
JOURNAL Patent: US 5763575-A 3 09-JUN-1998;
FEATURES
source Location/Qualifiers
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/mol_type="unassigned DNA"

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DB	1	CGCTCCAGGCGCTGGTGTGACGACGACCTGTCTCATTAATTAATAATGAATGA		60
QY	61	TGTACTTTCATTTGAAACAAACAGTGTACTGTGAAACATTATTTCTGTAATGACCT		120
DB	61	TGTACTTTCATTTGAAACAAACAGTGTACTGTGAAACATTATTTCTGTAATGACCT		120
QY	121	TGTCTCTCTTCTTGTGACGAAACCAATGATCTCTTAAGGAAGAACCTTATTTGTTA		180
DB	121	TGTCTCTCTTCTTGTGACGAAACCAATGATCTCTTAAGGAAGAACCTTATTTGTTA		180
QY	181	GGTTGATGACATCCCAAGTCACTGGAAGAGTTACAGTTGAACAGTCTTCTGT		240
DB	181	GGTTGATGACATCCCAAGTCACTGGAAGAGTTACAGTTGAACAGTCTTCTGT		240
QY	241	GGATGATTTTTCGACATCTGTCTCACTGGAACACCACTGTCTTCTTCAATTTGT		300

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Db      241 GGATGAGTTTTCGACTGTCTCTCACTGAGAAACTGACCACTGTCTCTTCCAAATTG 300
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Db      301 CTACACAAATGTTGTGTGGTGGTTTGCAGATTAACGGATGAGCCCTGAGGCTTTTCT 360
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Db      361 TTTCCGAACCTAAGAGAGAGACCCCTGTCGTGATTTACATGAGCCAACTGAGCTTGA 420
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Db      421 CCTCTCTCTGTGATCTGTGTTCCCTTTGAAGATTTGCTTATCAATACATGAGCAACTG 480
QY      481 GATTTAAGGAGAAAGCTCTTTGTATGATGATGCTTATGAGCTTTTCTATGAGCAACTG 540
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Db      601 GGGGCACTCCAGAGAAAGAGCAAACTTGCATTTGGCATTTCCCTGGCAATATGAGCTGCT 660
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Db      661 GATTTCGTGTGATCACTCCCTTTGTATGATGATGCTGAGAGACCAATCTTCACTTCCCT 720
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Db      781 TTAATCTCTCTCTCTGAGCACTTGGGCTTTTCTGTTCCAGCCCTTCTCAACCTCTGCTG 840
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Db      901 AAGAGAGAGGAGGAGCACTCAATGCTGATGCTGAGGATGCTGAGGATGCTGAGGATGCT 960
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Db      1021 TGTCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
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Db      1141 CCGAATGTCCTGAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
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Db      1201 GAATTCAGAGCTCTTACTCTTCAAGTTCAACCACTGTTAAGACCTCTATTGAGTT 1255

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RESULT 2
LOCUS   AR171258
DEFINITION Sequence 3 from patent US 6297026.
ACCESSION AR171258
VERSION  AR171258.1 GI:17910208

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1255)
AUTHORS     Sundelin, J. and Scarborough, R. M.
TITLE        Nucleic acids encoding the C140 receptor
JOURNAL      Patent: US 6297026-A 3 02-OCT-2001;
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      61 TGTACTTTTCAATTTGAACAAACCAAGTGTACTGTGAAAATTTATTTCTGTATGACCT 120
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QY      181 GGTGTATGACATCCCACTGCACTGAAAAGAGTTACATGTTGAACAGTCTTTTCTGT 240
Db      181 GGTGTATGACATCCCACTGCACTGAAAAGAGTTACATGTTGAACAGTCTTTTCTGT 240
QY      241 GGATGAGTTTTCGATCTGTCTCTCACTGAGAAACCTGACACGCTTCTTCCAAATGT 300
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QY      301 CTACACAAATGTTGTGTGGTGGTTTGCAGATTAACGGATGAGCCCTGAGGCTTTTCT 360
Db      301 CTACACAAATGTTGTGTGGTGGTTTGCAGATTAACGGATGAGCCCTGAGGCTTTTCT 360
QY      361 TTTCCGAACCTAAGAGAGAGACCCCTGTCGTGATTTACATGAGCCAACTGAGCTTGA 420
Db      361 TTTCCGAACCTAAGAGAGAGACCCCTGTCGTGATTTACATGAGCCAACTGAGCTTGA 420
QY      421 CCTCTCTCTGTGATCTGTGTTCCCTTTGAAGATTTGCTATACATGAGCAACTG 480
Db      421 CCTCTCTCTGTGATCTGTGTTCCCTTTGAAGATTTGCTATACATGAGCAACTG 480
QY      481 GATTTAAGGAGAAAGCTCTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db      481 GATTTAAGGAGAAAGCTCTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 540
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Db      541 TTCCATTTCTTTGATGACCTGCTCAGTGTGAGAGGATTTGGGTCAATGCTGAACCCAT 600
QY      601 GGGGCACTCCAGAGAAAGAGCAAACTTGCATTTGGCATTTCCCTGGCAATATGAGCTGCT 660
Db      601 GGGGCACTCCAGAGAAAGAGCAAACTTGCATTTGGCATTTCCCTGGCAATATGAGCTGCT 660
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Db      661 GATTTCGTGTGATCACTCCCTTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY      721 GAACATACGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db      721 GAACATACGACCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY      781 TTAATCTCTCTCTCTGAGCACTTGGGCTTTTCTGTTCCAGCCCTTCTCAACCTCTGCTG 840
Db      781 TTAATCTCTCTCTCTGAGCACTTGGGCTTTTCTGTTCCAGCCCTTCTCAACCTCTGCTG 840

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[illegible]

RESULT 3			
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LOCUS	142455	1255 bp	DNA
DEFINITION	Sequence 3 from patent US 5625174.		linear
			PAT 07-OCT-1997

Source	Organism
Unknown.	Unknown.
Unknown.	Unknown.

REFERENCE	1 (bases 1 to 1255)
AUTHORS	Sundelin, J. and Seatonrough, R.M.
TITLE	Recombinant C140 receptor
JOURNAL	Patent: US 5629174-A 3 13-MAY-1997
FEATURES	Location/Qualifiers
SOURCE	1..1255

ORIGIN

Query Match	100.0%	Score 1255;	DB 6;	Length 1255;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1255; Conservative	0;	Mismatches	0;	Gaps 0;

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Qy	61	TGTACTTTCATTTGAACAAAACCAAGTTACTGTGAAAATTTATTTCTGTATGACCT	120
Db	61	TGTACTTTCATTTGAACAAAACCAAGTTACTGTGAAAATTTATTTCTGTATGACCT	120
Qy	121	TGTCCTCCCTTCTGTACAGGAACCAATAGATCCTCTAAAGAAAGAACCTTATTTGTTA	180
Db	121	TGTCCTCCCTTCTGTACAGGAACCAATAGATCCTCTAAAGAAAGAACCTTATTTGTTA	180
Qy	181	GATTATGCGACATCCCACTCACTGAGAAAAGAGTTACAGTTGAAAACAGCTTTTCTGT	240
Db	181	GATTATGCGACATCCCACTCACTGAGAAAAGAGTTACAGTTGAAAACAGCTTTTCTGT	240
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Db	241	GGAATGAGTTTCTGCATCTGTCTCTCACTGAGAAAATGACCACTGTCTTCTTCCAAATGT	300

QY	301	CTACACAAATGTTGTTTGGTGGGGTTTGGCCAAAGTAAGGGATGGCCCTGGTGGGCTTTCT	360
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QY	481	GATTTAAGGGGAACCTCTTTGTATATGTGACTTATGGCTTTTTCATATGGCAACATGTACTG	540
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Db	601	GGGGCACTCCAGAAAGAAAGCAAAATTTGCCATTTGSGCATCTCCCTGGCAATATGGCTGCT	660
QY	661	GATTTCTGTGTGATCAACATCCCTTTGTATATGTGTGAAGACAAACCATCTTCAATTCCTGGCCT	720
Db	661	GATTTCTGTGTGATCAACATCCCTTTGTATATGTGTGAAGACAAACCATCTTCAATTCCTGGCCT	720
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QY	1201	GAATTCAGAGCTCTTAATCTTCAAGTTCAACCACTGTTTAAACCTCCTCATTTGAAGTT	1255
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RESULT 4					
LOCUS	187849				
DEFINITION	187849	Sequence 3 from patent	1255 bp	DNA	linear
ACCESSION	187849				
VERSION	187849.1	GI:340789			
KEYWORDS	.				
					PAT 10-AUG-1998

SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 1255)
 TITLE Sundelin, J. and Scarborough, R.M.
 METHOD Method to determine ligands, agonist and antagonist of C140
 receptor.
 JOURNAL Patent: US 5716789-A 3 10-FEB-1998;
 FEATURES Location/Qualifiers
 source 1..1255
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ORIGIN

Query Match 100.0%; Score 1255; DB 6; Length 1255;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1255; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCTCCAGGCTGGGTGACAGGAGACCTGTCTCATTAATTAATAATGAATGA 60
 DB 1 CGCTCCAGGCTGGGTGACAGGAGACCTGTCTCATTAATTAATAATGAATGA 60
 QY 61 TGTACTTTGATTTGAACAACAGTGTTCCTGCTAAACATTTATTTCTGTATGACCT 120
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 QY 1201 GAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTAAAGACTCTCTATTGAGTT 1255
 DB 1201 GAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGTAAAGACTCTCTATTGAGTT 1255

RESULT 5
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 LOCUS Homo sapiens coagulation factor II (thrombin) receptor-like 1
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 ACCESSION AF400075
 VERSION AF400075.1 GI:15021772
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;
 MAMMALIA; BUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
 REFERENCE 1 (bases 1 to 18351)
 AUTHORS Rieder, M.U., Carrington, D.P., Chung, M.-W., Lee, K.L., Poel, C.L.,
 Yi, Q. and Nickerson, D.A.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-2001) Molecular Biotechnology, University of
 Washington, 1705 NE Pacific, Seattle, WA 98195, USA
 COMMENT To cite this work please use: SeattleSNPs, NHBI Program for
 Genomic Applications, UW-FHCRC, Seattle, WA (URL:
 http://pga.mbl.washington.edu)
 This sequence consists of 2 contigs. The gap between the contigs
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 10775 10874: gap of unknown length
 10875 18351: contig of 7477 bp in length.
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Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 6
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LOCUS 107278 bp DNA linear PRI 05-NOV-2002
DEFINITION Homo sapiens chromosome 5 clone RP11-206N2, complete sequence.
ACCESSION AC114962
VERSION AC114962.2 GI:24580362
KEYWORDS HTG.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 107278)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submissions
JOURNAL Unpublished
2 (bases 1 to 107278)
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submissions
JOURNAL Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 107278)
REFERENCE
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submissions
JOURNAL Submitted (05-NOV-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Nov 5, 2002 this sequence version replaced gi:19424423.
COMMENT
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.2.
NOTE: This insert is not the entire sequence of the clone (entire
sequence is 201,6kb). It is clipped at the overlaps with AC027342
and AC010621. The number of bases overlapped with AC027342 is 5439
and with AC010621 is 28528.
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[illegible]

Sequencing vector: M13; M77815; 100% of reads

Center/Mittelead Institute/ MIT Center for Genome Research
Center code: MIBR
Web site: <http://www-seg.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
Project information
Center project name: L5802
Center clone name: 206_N_2
Summary Statistics
Sequencing vector: M13/ M7815, 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167659 bases at least Q40
Consensus quality: 175736 bases at least Q30
Consensus quality: 178914 bases at least Q20
Insert size: 154000; agarose-fp
Insert size: 180936; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 37 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1255 2766: contig of 1512 bp in length
* 2767 2866: gap of 100 bp
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* 5192 5292: gap of 100 bp
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* 7388 7487: gap of 100 bp
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Matches 1247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 66654 TTTCTGATCTGTCTCTCACTGTAAGAAAGTGAACCACTGTCTTCTTCAATGTCTACA 66595

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RESULT 8

AC010621 52368 bp DNA linear PRI 26-JAN-2002

LOCUS Homo sapiens chromosome 5 clone CTD-2034J20, complete sequence.

DEFINITION AC010621

VERSION AC010621.7 GI:18376859

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 52368)

DOE Joint Genome Institute and Stanford Human Genome Center.

2 (bases 1 to 52368)

DOE Joint Genome Institute.

3 (bases 1 to 52368)

Submitted (16-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

REFERENCE

DOE Joint Genome Institute and Stanford Human Genome Center.

Submitted (26-JAN-2002) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jan 26, 2002 this sequence version replaced gi:13699549.

Draft Sequence Produced by DOE Joint Genome Institute

COMMENT

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.sngc.stanford.edu

Quality: Phrap Quality >=40 99.4% of Sequence;

Estimated Total Number of Errors is 0.2.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 142.2kb). It is clipped at the overlap with AC025188.

The number of bases overlapped is 12615.

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Location/Qualifiers

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ORIGIN

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Best Local Similarity 99.8%; Pred. No. 0;

Matches 1245; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 43466 CATTGGAACAAACAGGTGATGCTGTAACATTTATTTCTGTATAGACCTGTCTCC 43525

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DEFINITION BP).
ACCESSION Z49994
VERSION Z49994.1 GI:1008086
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1289)
AUTHORS Nystedt,S., Emilsson,K., Larsson,A.K., Strombeck,B. and Sundelin,J.
TITLE Molecular cloning and functional expression of the gene encoding
the human proteinase-activated receptor 2
JOURNAL Eur. J. Biochem. 232 (1), 84-89 (1995)
MEDLINE 96048032
PUBMED 7561175
REFERENCE 2 (bases 1 to 1289)
AUTHORS Nystedt,S.
TITLE Direct Submision
JOURNAL Submitted (03-JUL-1995) Sverker Nystedt, Division of Neurobiology,
The Wallenberg, Laboratory, Lund University, Soelvegatan 33A, Lund,
S-223 62, Sweden

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Matches 1211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 12186 from Patent WO02068579.
ACCESSION C0726252
VERSION C0726252.1 GI:42288766
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Mammalia; Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.
AUTHORS

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TITLE Rle, such as nucleic acid arrays, comprising a majority of
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JOURNAL Patent: WO 02068579-A 12186 06-SEP-2002;
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 VERSION BC012453.1 GI:15214649
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 2813)
 AUTHORS Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Hsieh F.,
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 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L.,
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 Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J.,
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 Wierley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S.,
 Sanchez A., Whiting M., Madan A., Young A.C., Shcherbako Y.,
 Bouffard G.G., Blakeley R.W., Touchman D.W., Green E.D.,
 Dickson M.C., Rodriguez A.C., Grimwood J., Schultz J., Myers R.M.,
 Butterfield Y.S., Krzywinski M.I., Skalska U., Smallius D.E.,
 Scherch A., Schein J.E., Jones S.J. and Marra M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
 JOURNAL
 PUBLISHED
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 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT

2 (bases 1 to 2813)
 Strausberg, R.
 Direct Submissions
 Submitted (15-AUG-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-rt@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LMLN)
 Sequencing Center
 Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu X., Hulyk, S.W., Louieged, R.,
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
 A.N., Gibbs, R.A.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LMLN at: <http://image.llnl.gov>
 Series: IRMA Plate: 21 Row: B Column: 20
 This clone was selected for full length sequencing because it
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QY	1099	TTCACATGATTTTCAAGGATCATGCAAGAAAGCTCTCTTGTGCGAAGTGTCCGACCTGT	1158		
DB	1195	TTCACATGATTTTCAAGGATCATGCAAGAAAGCTCTCTTGTGCGAAGTGTCCGACCTGT	1254		
QY	1159	AATGAGATGCAAGTATCCCTCACTCAAGAAAGAACTCCAGGAAATCCAGCTCTTACTC	1218		

DB	1255	AAGCAGATGCAAGTATCCCTCACTCAAGAAAGAACTCCAGGAAATCCAGCTCTTACTC	1314		
QY	1219	TTCAAGTTCAACCACTGTTAAGACCTCTATTGAGTT	1255		
DB	1315	TTCAAGTTCAACCACTGTTAAGACCTCTATTGAGTT	1351		
RESULT 13					
AY336105					
LOCUS	1275 bp	mRNA	linear	PRI 28-JUL-2003	
DEFINITION	Homo sapiens	protease-activated receptor 2 (PAR2)	mRNA, complete		
ACCESSION	AY336105				
VERSION	AY336105.1	GI:33149991			
KEYWORDS					
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Luo, W., Sedehezade, F., Hanck, T. and Reiser, G.				
TITLE	1 (bases 1 to 1275)				
JOURNAL	Human protease-activated receptor 2 (PAR-2)				
REFERENCE	2 (bases 1 to 1275)				
AUTHORS	Luo, W., Sedehezade, F., Hanck, T. and Reiser, G.				
TITLE	Submitted (04-JUL-2003) Medical Faculty, Institute of Neurobiochemistry, Leipziger Str. 44, Magdeburg, Saxony-Anhalt 39120, Germany				
JOURNAL					
FEATURES					
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	/map="5q13"				
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	/note="synonym: PAR2"				
	82..1275				
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	/note="G-protein-coupled receptor; PAR-2"				
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	/protein_id="AAP97012.1"				
	/db_xref="GI:33149992"				
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ORIGIN					
Query Match	88.8%;	Score 1114;	DB 9;	Length 1275;	
Best Local Similarity	100.0%;	Pred. No. 5.1e-305;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 1114;	Conservative 0;				
QY	139	AGGACCAATAGATCTCTAAGAGAAAGCCCTTATGTGAAGTTGATGGACATCCCA	198		
DB	162	AGGACCAATAGATCTCTAAGAGAAAGCCCTTATGTGAAGTTGATGGACATCCCA	221		
QY	199	CGTCACTGAGAAAGATTACAGTTGAAACAGCTTTTCTGTGATGAGATTTTCTGCATC	258		
DB	222	CGTCACTGAGAAAGATTACAGTTGAAACAGCTTTTCTGTGATGAGATTTTCTGCATC	281		
QY	259	TGTCTCACTGAGAAAGATTACAGTTGATTTCTCAATTTGCTACAAATGTTTGT	318		
DB	282	TGTCTCACTGAGAAAGATTACAGTTGATTTCTCAATTTGCTACAAATGTTTGT	341		

QY 319 GGTGGGTTTCCAGTAACGGCATGCGCCCTGTGGGCTTTCTTTCCGAATAAGAA 378
 DB 342 GGTGGGTTTCCAGTAACGGCATGCGCCCTGTGGGCTTTCTTTCCGAATAAGAA 401
 QY 379 GCAACCTGTGTGATTTACATAGCCAACTGGCCTTGGCTGACCTCTCTGTCACTG 438
 DB 402 GCAACCTGTGTGATTTACATAGCCAACTGGCCTTGGCTGACCTCTCTGTCACTG 461
 QY 439 GTTCCCTTGAAGATTTGCTTATCATACATATGGAACAACCTGATTTATAGGAAAGCTCT 498
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 QY 499 TTGTAATGTGCTTATTTGCTTATTTCTATGGAACAATGTAATGTCATTTCTTCATGAC 558
 DB 522 TTGTAATGTGCTTATTTGCTTATTTCTATGGAACAATGTAATGTCATTTCTTCATGAC 581
 QY 559 CTGCTCTAGTGTGCAAGAGTATTTGGATCATGTGAACCCCAATGGGGAATTCAGAAAGAA 618
 DB 582 CTGCTCTAGTGTGCAAGAGTATTTGGATCATGTGAACCCCAATGGGGAATTCAGAAAGAA 641
 QY 619 GGGAAACATTTGCCATTTGGCATTTCCCTGGCAATATGCTGTGATTTCTGCTGTCAACAT 678
 DB 642 GGGAAACATTTGCCATTTGGCATTTCCCTGGCAATATGCTGTGATTTCTGCTGTCAACAT 701
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 DB 702 CCTTTGTATGTGTGAAGAGACCATCTTCAATTCCTGACCTGAACATCAAGACCTGTCA 761
 QY 739 TGAATTTTGGCTGAGAGAGCTTTGTGTGGAGACATGTTCAATTAATCTCTCTGTGAC 798
 DB 762 TGAATTTTGGCTGAGAGAGCTTTGTGTGGAGACATGTTCAATTAATCTCTCTGTGAC 821
 QY 799 CATTTGGGCTTTTCTGTTCCTCAAGCTTCTCTCAAGCTCTGTGCTTATGTGTGATGATCAG 858
 DB 822 CATTTGGGCTTTTCTGTTCCTCAAGCTTCTCTCAAGCTCTGTGCTTATGTGTGATGATCAG 881
 QY 859 AATGCTGCGATCTTCTGSCCATGATGAACTGAGAACTGAGAAAGAAAGAGGCGCATCAA 918
 DB 882 AATGCTGCGATCTTCTGSCCATGATGAACTGAGAACTGAGAAAGAAAGAGGCGCATCAA 941
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 DB 1002 TGTGTGTGATTTATTTTCTGATTAAGAGCCAGGCGCAAGGCAATGTCTATGCTGTATCAT 1061
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 DB 1062 TGTAGCCCTGTGCTCTTACCCCTTAACAGTGTGATGAGACCCCTTGTCTATTAATCTTGT 1121
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 DB 1122 TTGCAATGATTTCAAGGATCATGCAAGAAAGAGCTCTCTTGTGCGAAGTGTCCGCACTGT 1181
 QY 1159 AAGGCAATGCAAGATTCCTCTCACTCAAGAAAGAACTCCAGGAATTCAGCTCTTACTC 1218
 DB 1182 AAGGCAATGCAAGATTCCTCTCACTCAAGAAAGAACTCCAGGAATTCAGCTCTTACTC 1241
 QY 1219 TTCAAGTTCAACACCTGTAAAGACCTCTTATTTGA 1252
 DB 1242 TTCAAGTTCAACACCTGTAAAGACCTCTTATTTGA 1275

RESULT 14
 LOCUS CO870621 1451 bp DNA
 DEFINITION Sequence 30 from Patent WO2004073657.
 ACCESSION CO870621
 VERSION CO870621.1 GI:52000132
 KEYWORDS
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Aiz,N., Gish,K.C., Wilson,K.E. and Zlotnik,A.
 TITLE Methods of diagnosis of cancer, composition and methods of
 screening for modulators of cancer
 JOURNAL Patent: WO 2004073657-A 30 02-SEP-2004;
 PROTEIN DESIGN LABS, INC. (US)
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 Best Local Similarity 99.8%; Pred. No. 6e-305;
 Matches 1115; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 139 AGGAACCAATGATTCCTTAAAGAAAGCCCTTATTTGTAAGTTGATGGCAATGCCA 198
 DB 228 AGGAACCAATGATTCCTTAAAGAAAGCCCTTATTTGTAAGTTGATGGCAATGCCA 287
 QY 199 CGTCACTGAAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGGATGAGTTTCTGTGATC 258
 DB 288 CGTCACTGAAAAAGAGTTACAGTTGAAACAGTCTTTCTGTGGATGAGTTTCTGTGATC 347
 QY 259 TGTCTCACTGAAAACTGACCACTGCTTCTTCAATTTGTGTACAAATGTTGT 318
 DB 348 TGTCTCACTGAAAACTGACCACTGCTTCTTCAATTTGTGTACAAATGTTGTGT 407
 QY 319 GGTGGGTTTCCAGTAACGGCATGCGCCCTGTGGGCTTTCTTTCCGAATAAGAA 378
 DB 408 GGTGGGTTTCCAGTAACGGCATGCGCCCTGTGGGCTTTCTTTCCGAATAAGAA 467
 QY 379 GCAACCTGTGTGATTTACATAGCCAACTGGCCTTGGCTGACCTCTCTGTCACTG 438
 DB 468 GCAACCTGTGTGATTTACATAGCCAACTGGCCTTGGCTGACCTCTCTGTCACTG 527
 QY 439 GTTCCCTTGAAGATTTGCTTATGCAATATGGAACCCCAATGGGGAATTCAGAAAGCTCT 498
 DB 528 GTTCCCTTGAAGATTTGCTTATGCAATATGGAACCCCAATGGGGAATTCAGAAAGCTCT 587
 QY 499 TTGTAATGTGCTTATTTGCTTATTTCTATGGAACAATGTAATGTCATTTCTTCATGAC 558
 DB 588 TTGTAATGTGCTTATTTGCTTATTTCTATGGAACAATGTAATGTCATTTCTTCATGAC 647
 QY 559 CTGCTCTAGTGTGCAAGAGTATTTGGATCATGTGAACCCCAATGGGGAATTCAGAAAGAA 618
 DB 648 CTGCTCTAGTGTGCAAGAGTATTTGGATCATGTGAACCCCAATGGGGAATTCAGAAAGAA 707
 QY 619 GGGAAACATTTGCCATTTGGCATTTCCCTGCAATATGAGCTGATTTCTGTGTCAACAT 678
 DB 708 GGGAAACATTTGCCATTTGGCATTTCCCTGCAATATGAGCTGATTTCTGTGTCAACAT 767
 QY 679 CCTTTGTATGTGTGAAGAGACCATTTCAATTCCTGACCTGAACATCAAGACCTGTCA 738
 DB 768 CCTTTGTATGTGTGAAGAGACCATTTCAATTCCTGACCTGAACATCAAGACCTGTCA 827
 QY 739 TGAATTTTGGCTGAGAGAGCTTTGTGTGGAGACATGTTCAATTAATCTCTCTGTGAC 798
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Db 1248 AAAGCAGATGCAAGTATCCCTCACCTCAAGAAACTCCAGGAAATCCAGCTCTTACTC 1307
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Db 1308 TTCAGTTCAACCACTGTTAAGACTCTCTATTGAGTT 1344

RESULT 15
CQ876755 1451 bp DNA linear PAR 04-OCT-2004
LOCUS CQ876755
DEFINITION Sequence 1 from Patent WO2004080373.
ACCESSION CQ876755
VERSION CQ876755.1 GI:53790207
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1
Golz,S., Brueggemeier,U. and Summer,H.
Diagnosics and therapeutics for diseases associated with g-protein
coupled proteinase activated receptor 2 (par2)
Patent: WO 2004080373-A 1 23-SEP-2004;
Bayer Healthcare AG (DE)
location/Qualifiers
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ORIGIN
Query Match 88.7%; Score 1113.8; DB 6; Length 1451;
Best Local Similarity 99.8%; Pred. No. 6e-305; Indels 0; Gaps 0;
Matches 1115; Conservative 0; Mismatches 2;

Qy 139 AGGACCAATATGATCTCTTAAGAGAGCCCTTATGTAAGTGTGAGCCATGCCA 198
Db 228 AGGACCAATATGATCTCTTAAGAGAGCCCTTATGTAAGTGTGAGCCATGCCA 287
Qy 199 CGTCACTGAAAAAGATTACAGTTGAAACAGCTTTTCTGTGATGAGTTTCTGCATC 258
Db 288 CGTCACTGAAAAAGATTACAGTTGAAACAGCTTTTCTGTGATGAGTTTCTGCATC 347
Qy 259 TGTCTCTCACTGAAAACTGACCACTGTCTTCTTCAATTGTCTACCAATTGTGTTGT 318
Db 348 TGTCTCTCACTGAAAACTGACCACTGTCTTCTTCAATTGTCTACCAATTGTGTTGT 407
Qy 319 GGTGGGTTTGGCAAGTAAGGCAATGGCCCTGTGGGTCTTCTTTCGAACTAAGAA 378
Db 408 GGTGGGTTTGGCAAGTAAGGCAATGGCCCTGTGGGTCTTCTTTCGAACTAAGAA 467
Qy 379 GCAACCTGTGATTTACATGAGCAATGAGCTTGGCTGACCTCTCTGTCACTG 438
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Qy 439 GTTCCCTTGAAAGATTGCTTATCATATACATGAGCAACACTGATTTATGGGAAGCTCT 498

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Qy 619 GGCAAACTTTGCAATTTGGCATCTCCCTGGCAATATGGGCTGATTTCTGCTGATCCAT 678
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Qy 679 CCTTTGTATGTGCTGAACAGACCAATCTTCAATTCCTGCTGAAATCATGACGACCTGTCA 738
Db 768 CCTTTGTATGTGCTGAACAGACCAATCTTCAATTCCTGCTGAAATCATGACGACCTGTCA 827
Qy 739 TGAATGTTTGGCTTGAGACGCTCTTGGTGGAGACATGTTCAATTACTTCTCTCTGCG 798
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Qy 799 CATGGGGTCTTTCTGTTCCAGCCTTCTCTCAAGCTCTGCTATGCTGATGATGAC 858
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Qy 919 ACTGATTTGACTGTCTGCGCATGTATCTGATCTGCTTCACTCTCTATGTAACCTTCTGCT 978
Db 1008 ACTGATTTGACTGTCTGCGCATGTATCTGATCTGCTTCACTCTCTATGTAACCTTCTGCT 1067
Qy 979 TGTGTGTCATTAATTTCTGATTAAGAGCCAGAGCCAGATGTCATATGCCCTGTACAT 1038
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Qy 1099 TTCACATGATTTAGGATATGCAAGAAAGCTCTCTTGGCCGAAGTCCGCACTGT 1158
Db 1188 TTCACATGATTTAGGATATGCAAGAAAGCTCTCTTGGCCGAAGTCCGCACTGT 1247
Qy 1159 AAAGCAGATGCAAGTATCCCTCACCTCAAGAAACTCCAGGAAATCCAGCTCTTACTC 1218
Db 1248 AAAGCAGATGCAAGTATCCCTCACCTCAAGAAACTCCAGGAAATCCAGCTCTTACTC 1307
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Db 1308 TTCAGTTCAACCACTGTTAAGACTCTCTATTGAGTT 1344

Search completed: March 21, 2005, 21:39:45
Job time : 5676.07 secs

XX Scarbrough RM, Sundelin J;
 XX WPI; 1995-075182/10.
 DR N-PSDB; AA084558.
 XX
 PT New DNA encoding recombinant C140 receptor - and novel agonists and
 PT antagonists and specific antibodies with therapeutic and diagnostic
 PT applications.
 XX
 PS Disclosure; Fig 2; 57pp; English.
 CC The availability of genomic DNA encoding the mouse protease C140 receptor
 CC (see Q84557) permitted the retrieval of the corresp. human gene. A human
 CC genomic library cloned in the vector EMBL3 was screened using the entire
 CC coding region of the murine clone as a probe. The recovered human gene
 CC including the DNA sequence and the deduced AA sequence are shown in
 CC Q84558 & R68921. Subsequent experiments indicated that the human C140
 CC gene is located in the same region of the long arm of chromosome number 5
 CC (5q12-5q13) as has been reported for the human thrombin receptor gene.
 CC (Updated on 25-MAR-2003 to correct PM field.)
 CC
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2030; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 5,6e-210;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNVLSEQISVIAETPIVSWTLVFLSCTGNRSSKGRSLGKVDGSHVTKGVTVETVF 60
 DB 1 MNVLSEQISVIAETPIVSWTLVFLSCTGNRSSKGRSLGKVDGSHVTKGVTVETVF 60
 QY 61 SVDEFASVLTGKLTVPFLPIVYIVFVVGIPNGMALWFLFRTKKKHPAVIYMANIAL 120
 DB 61 SVDEFASVLTGKLTVPFLPIVYIVFVVGIPNGMALWFLFRTKKKHPAVIYMANIAL 120
 QY 121 ADLSTVWPEPLKTAHYHGNMWTYGEALCNVLIGFFYGNMYSILFPTCLSVORVYIVN 180
 DB 121 ADLSTVWPEPLKTAHYHGNMWTYGEALCNVLIGFFYGNMYSILFPTCLSVORVYIVN 180
 QY 181 PMGSHRKNIAIGISLAIWLLVLTPIVYVKKPTFPALMTTCCHDLPBOLLVGM 240
 DB 181 PMGSHRKNIAIGISLAIWLLVLTPIVYVKKPTFPALMTTCCHDLPBOLLVGM 240
 QY 241 FNFELSLAIGVFLPAPLFTASAVYLMIRMLRSAMDENSEKRRRAIKLIVTLAMYLIC 300
 DB 241 FNFELSLAIGVFLPAPLFTASAVYLMIRMLRSAMDENSEKRRRAIKLIVTLAMYLIC 300
 QY 301 FTFSNLLLVHYFLIKSQGSHVYALYVALCLSTNSCIDPVTYTFVSHDFDHAKNAL 360
 DB 301 FTFSNLLLVHYFLIKSQGSHVYALYVALCLSTNSCIDPVTYTFVSHDFDHAKNAL 360
 QY 361 LCRSVRTVKOMQVSLTSKHSRSSSSSTTVKTSY 398
 DB 361 LCRSVRTVKOMQVSLTSKHSRSSSSSTTVKTSY 398
 RESULT 2
 AA01953
 ID AA01953 standard; protein; 398 AA.
 XX
 AC AA01953;
 XX
 DT 01-APR-1997 (first entry)
 XX
 DE Human C140 receptor, with putative signal sequence.
 XX
 XX C140 receptor; G-protein linked; coupled; seven pass; agonist;
 KM antagonist; hypertension; hypotension; blood pressure.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Peptide 1..27
 FT /note= "putative signal peptide, differs from signal
 FT peptide encoded by a cDNA clone of this receptor (see
 FT AA01955), the signal sequence given for the cDNA clone
 FT is believed to be the correct sequence"
 FT 28..398
 FT Protein
 FT /note= "mature protein"
 FT 31
 FT Modified-site
 FT /note= "potential Asn-linked glycosylation site"
 FT 37..38
 FT Cleavage-site
 FT /note= "putative protease receptor cleavage site"
 FT 81..103
 FT Region
 FT /note= "transmembrane region I"
 FT 111..132
 FT Region
 FT /note= "transmembrane region II"
 FT 151..174
 FT Region
 FT /note= "transmembrane region III"
 FT 191..212
 FT Region
 FT /note= "transmembrane region IV"
 FT 223
 FT Modified-site
 FT /note= "potential Asn-linked glycosylation site"
 FT 245..267
 FT Region
 FT /note= "transmembrane region V"
 FT 289..309
 FT Region
 FT /note= "transmembrane region VI"
 FT 327..348
 FT Region
 FT /note= "transmembrane region VII"
 XX
 PN W09623225-A1.
 XX
 XX 01-AUG-1996.
 PD
 XX
 PF 25-JAN-1996; 96WO-US001179.
 XX
 PR 25-JAN-1995; 95US-00390301.
 XX
 PA (COR-) COR THERAPEUTICS INC.
 XX
 PI Sundelin J, Scarbrough RM;
 XX
 DR WPI; 1996-362813/36.
 DR N-PSDB; AAT32037.
 XX
 PT Vector for expression C140 cell surface receptor in host cell - useful to
 PT identify C140 agonist and antagonists, which are antihypertensives and
 PT elevators of blood pressure, respectively.
 XX
 PS Example 2; Fig 2A-B; 60pp; English.
 XX
 CC AA01953 represents the human C140 receptor (C140R), including a putative
 CC signal peptide (see features table). DNA encoding C140R may be engineered
 CC so as to allow the recombinant expression of C140R in a suitable host
 CC cell, i.e. by removing the native expression-control sequences and
 CC replacing them with control sequences operable in the host. Such a
 CC recombinant receptor can be expressed on the surface of oocytes, this
 CC provides a good assay system for identifying agonists/antagonists of
 CC C140R. The C140 receptor is a G-protein linked receptor and a member of
 CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
 CC transmembrane regions within the cell membrane seven times, producing seven
 CC involved in controlling blood pressure. C140 antagonists (see AA01942-
 CC W01951) are useful to inhibit signalling from this receptor, resulting in
 CC an increase in blood pressure and are therefore useful in pharmaceuticals
 CC for the treatment of hypotension (low blood pressure). Conversely
 CC agonists (see AA01941-W01941) of C140 are useful in pharmaceuticals for
 CC the treatment of hypertension (high blood pressure)
 XX
 SQ Sequence 398 AA;
 Query Match 100.0%; Score 2030; DB 2; Length 398;
 Best Local Similarity 100.0%; Pred. No. 5,6e-210;
 Matches 398; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTLSPEQTSVTAETPFISVMTLVPLSCGTGTRSSKGRSLIGKVDGTSHTGKGVTEVTF 60
 DB 1 MNTLSPEQTSVTAETPFISVMTLVPLSCGTGTRSSKGRSLIGKVDGTSHTGKGVTEVTF 60
 QY 61 SYDEFSASVLTGKLTIVFPVIVTVIVFVGLPSNGMALWVLFRTKKKGPVIMANLAL 120
 DB 61 SYDEFSASVLTGKLTIVFPVIVTVIVFVGLPSNGMALWVLFRTKKKGPVIMANLAL 120
 QY 121 ADLLSVTWPLKTAHYHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVN 180
 DB 121 ADLLSVTWPLKTAHYHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVN 180
 QY 121 ADLLSVTWPLKTAHYHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVN 180
 DB 121 ADLLSVTWPLKTAHYHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVN 180
 QY 181 PMGSHRKANAIAGISLAWLILVTIPLYVVKQTFIPALNITTCVDLPBQLVGDGM 240
 DB 181 PMGSHRKANAIAGISLAWLILVTIPLYVVKQTFIPALNITTCVDLPBQLVGDGM 240
 QY 241 FNYFLSLAIGVLPFPAFLTASAVYLMIRLSSAMDENSEKKRRAIKLIVTLAMYLIC 300
 DB 241 FNYFLSLAIGVLPFPAFLTASAVYLMIRLSSAMDENSEKKRRAIKLIVTLAMYLIC 300
 QY 301 FTSSNLLLVHYHPLIKSGQSHVYALYVALCLSTLNSCIDPFVYVFSHPDHDHAKNAL 360
 DB 301 FTSSNLLLVHYHPLIKSGQSHVYALYVALCLSTLNSCIDPFVYVFSHPDHDHAKNAL 360
 QY 361 LCRSVRTVKOMOVSLTSKSKSRKSSSYSSSTTVKTSY 398
 DB 361 LCRSVRTVKOMOVSLTSKSKSRKSSSYSSSTTVKTSY 398

RESULT 3

AAB35641
 ID AAB35641 standard; protein: 397 AA.

AC AAB35641;

DT 19-FEB-2001 (first entry)

DE Human PAR-2 protein.

XX PAR-2; protease activated receptor-2; ECL-2; inflammatory disease;
 XX asthma; chronic obstructive pulmonary; arthritis; inflammatory bowel;
 XX psoriasis; eczema; multiple sclerosis.

OS Homo sapiens.

PN W0200063371-A1.

PD 26-OCT-2000.

PP 17-APR-2000; 2000MO-GB001455.

PR 15-APR-1999; 99GB-00008513.

PA (UYSO-) UNIV SOUTHAMPTON.

PI Walls AP, Palmer K, Compton SJ, Cairns JA, Gough AC;

DR WPI, 2000-679599/66.

PT Protease activated receptor 2 variants useful for treating inflammatory
 PT diseases such as asthma, arthritis and psoriasis, and as hyperensives,
 PT has reduced sensitivity to trypsin.

PS Claim 2, Page 55, 59pp; English.

XX The present invention relates to a variant protease activated receptor 2
 CC (PAR-2). The invention is useful for identifying an individual having a
 CC polymorphism in the ECL-2 region of one or both PAR-2 gene alleles. The
 CC invention may be used to develop treatments for inflammatory diseases
 CC such as asthma, chronic obstructive pulmonary disease, arthritis,
 CC inflammatory bowel diseases, psoriasis and eczema, multiple sclerosis and
 CC to raise blood pressure

SQ Sequence 397 AA;

Query Match 93.7%; Score 1903; DB 3; Length 397;
 Best Local Similarity 96.9%; Pred. No. 2.9e-196;
 Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1;

QY 18 SVMTLVPLSCGTGTRSSKGRSLIGKVDGTSHTGKGVTEVTFPSVDEFSASVLTGK 73
 DB 13 AILMAASLSCSGTIGTRSSKGRSLIGKVDGTSHTGKGVTEVTFPSVDEFSASVLTGK 72
 QY 74 LTTVPLPIVTVIVFVGLPSNGMALWVLFRTKKKGPVIMANLALADLLSVTWPLKI 133
 DB 73 LTTVPLPIVTVIVFVGLPSNGMALWVLFRTKKKGPVIMANLALADLLSVTWPLKI 132
 QY 134 AHHHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVNPMGSHRKANAI 193
 DB 133 AHHHGNMWTYGEALCNVLIGFPYGNMYCSILFMTCLSVORVYIVNPMGSHRKANAI 192
 QY 194 GISLAWLILVTIPLYVVKQTFIPALNITTCVDLPBQLVGDGMFNYFLSLAIGVFL 253
 DB 193 GISLAWLILVTIPLYVVKQTFIPALNITTCVDLPBQLVGDGMFNYFLSLAIGVFL 252
 QY 254 PPAFLTASAVYLMIRLSSAMDENSEKKRRAIKLIVTLAMYLICFTSSNLLLVHYF 313
 DB 253 PPAFLTASAVYLMIRLSSAMDENSEKKRRAIKLIVTLAMYLICFTSSNLLLVHYF 312
 QY 314 LKSGQSHVYALYVALCLSTLNSCIDPFVYVFSHPDHDHAKNALLCRSVRTVKOMOV 373
 DB 313 LKSGQSHVYALYVALCLSTLNSCIDPFVYVFSHPDHDHAKNALLCRSVRTVKOMOV 372
 QY 374 SLTSKSKSRKSSSYSSSTTVKTSY 398
 DB 373 SLTSKSKSRKSSSYSSSTTVKTSY 397

RESULT 4

AAB2678
 ID AAB2678 standard; protein: 397 AA.

AC AAB2678;

DT 13-DEC-2002 (first entry)

DE Human coagulation factor II (thrombin) receptor like 1 (F2RL1) protein.

XX Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
 XX polymorphism; chronic pulmonary disease; inflammatory disorder;
 XX gene therapy.

OS Homo sapiens.

PN W020025534-A2.

PD 18-JUL-2002.

PP 13-NOV-2001; 2001MO-US046475.

PR 10-NOV-2000; 2000US-0247516P.

PT (GENA-) GENAISSANCE PHARM INC.

PI Bieganski KM, Sanchis A, Shah N;

DR WPI, 2002-566728/60.

DR N-PSDB; AADA4437, AADA4438.

XX New genetic variants having polymorphisms in the coagulation factor II

PT (thrombin) receptor like 1 (F2RL1) gene, useful for studying the function

PT of F2RL1 and treating disorders associated with abnormal expression or function of F2RL1.

XX

PT Claim 27, Fig 3, 65pp, English.

PS

Claim 27; Fig 3; 65pp; English.

The invention relates to an isolated polynucleotide comprising genes and haplotypes of the coagulation factor II (thrombin) receptor like 1 (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in studying the expression and biological function of F2RL1, and in identifying drugs targeting F2RL1 protein for treating disorders associated with abnormal expression or function of F2RL1, e.g. asthma, chronic pulmonary disease, and inflammatory disorders. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular F2RL1 protein isoform, or an expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. Information on polymorphisms may be applied in studying biological functions of F2RL1 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The invention is useful in gene therapy. The present sequence is human F2RL1 protein

SQ Sequence 397 AA;

Query Match 93.7%; Score 1903; DB 5; Length 397;

Best Local Similarity 96.9%; Pred. No. 2.9e-196;
Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1.

QY	18	SWNTLVLEST----	GTNNSSKGRSLIGVDGTSHTGKGVVETVVFSDERSASVLTGK	73
		:::		
Db	13	AIILMASLSGSGIT	QGTNNSSKGRSLIGVDGTSHTGKGVVETVVFSDERSASVLTGK	72
QY	74	LTTVFLPIVYTVTVFVV	GLPDSNGMALWFLPRTKKGRPAVIYMANIALADLLSVIWFPLKI	133
Db	73	LTTVFLPIVYTVTVFVV	GLPDSNGMALWFLPRTKKGRPAVIYMANIALADLLSVIWFPLKI	133
QY	134	AHHHGNNTVYGEALCNVL	IGFPYGMNYSIIIPMTCLSYQRYWTVVPMGSKRKANITAI	197
Db	133	AHHHGNNTVYGEALCNVL	IGFPYGMNYSIIIPMTCLSYQRYWTVVPMGSKRKANITAI	197
QY	194	GISLAIWLLIILVITICLVYVKKQIF	IPALNITTCDDVLPBOLLVGDMDNVPFLSALIGFL	253
Db	193	GISLAIWLLIILVITICLVYVKKQIF	IPALNITTCDDVLPBOLLVGDMDNVPFLSALIGFL	253
QY	254	FPAPFLTASAVILMI	RMRSSAMDENSEKKRKRAIKLIYVLAMYLICTPSPNLLVHYHF	313
Db	253	FPAPFLTASAVILMI	RMRSSAMDENSEKKRKRAIKLIYVLAMYLICTPSPNLLVHYHF	313
QY	314	LIRSGQSHVYALYIVAL	CLSTLNSCIDPFVYVYVSHDPRDHAKNALLCRSVRYTKOMQV	373
Db	313	LIRSGQSHVYALYIVAL	CLSTLNSCIDPFVYVYVSHDPRDHAKNALLCRSVRYTKOMQV	373
QY	374	SLTSSKHRSKSSSYSSSS	STTVKTSY 398	
Db	373	SLTSSKHRSKSSSYSSSS	STTVKTSY 397	

RESULT 5
ABG73508
ID ABG73508 standard; protein; 397 AA

AC ABG73508;

DT 14-FEB-2003 (first entry)

DE Human par2 protein SEQ ID 39.

KM G-protein coupled receptor; HGPBMY1; HGPBMY2; immunosuppressive;
KM cardiant; neuroprotective; antiinflammatory; cytostatic; vulnerary;
KM vaccine; gene therapy; cardiovascular; neural; reproductive;

KM hematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
KM birth defect; aberrant phosphorylation; acute phase response; receptor;
KM signal transduction; hyperimmune activity; inflammatory; hypercongenital;
KM necrotic lesion; wound; organ transplant rejection.

OS Homo sapiens.

PN W0200268591-A2.

PD 06-SEP-2002.

PF 22-FEB-2002; 2002WO-US005281.

PR 23-FEB-2001; 2001US-0270792P.

PR 06-JUN-2001; 2001US-0296427P.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Feder J, Ramanathan C, Nelson

XX

X

PT preventing, treating or ameliorating a disorder e.g., wound,
PT cardiovascular disorder or transplant rejection.

PS Disclosure; Fig 4; 316pp; English.

CC This invention describes the novel human G-protein coupled receptors
CC (GPCR's), HGBRMY1 or HGBRMY2 which have immunosuppressive, cardiact,
CC neuroprotective, antiinflammatory, cytoprotastic and vulnary activity and
CC can be used in vaccines or for gene therapy. Pharmaceutical compositions
CC comprising HGBRMY1 or HGBRMY2 polypeptides or their agonists or
CC antagonists or modulators, or a HGBRMY1- or HGBRMY2-specific antibody
CC are useful for preventing, treating or ameliorating a medical condition
CC comprising autoimmune, cardiovascular, neural, reproductive,
CC haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
CC cell cycle or birth defect, a disorder related to aberrant
CC phosphorylation, acute phase responses or signal transduction or to
CC hyperimmune activity, an inflammatory or hypercongenital condition, a
CC necrotic lesion, a wound, organ transplant rejection or a condition
CC related to organ transplant rejection. This sequence represents a G-
CC protein coupled receptor associated with the human HGBRMY proteins
CC described in the disclosure of the invention

SQ Sequence 397 AA;

Query Match 93.7%; Score 1903; DB 6; Length 397;

Best Local Similarity 96.9%; Pred. No. 2.9e-196;
Matches 373; Conservative 4; Mismatches 4; Indels 4; Gaps 1.

Qy	18	SWTTLVFLSCT----	GINRSSKGRLLICKDQGTSHVNGKGLTVAEVPSVDEFSASVLTGK	73
		:::		
Db	13	AIILAAASLSCGTIGCTINRSSKGRSLIGKDQGTSHVTKAGVTVETVPSVDEFSASVLTGK		72
Qy	74	LTTVPFLPIYVTIVFVVGEPNSGMALMVEFLRTKKKHPAVITYMANIALADLLSVIPEPLKI		133
Db	73	LTTVPFLPIYVTIVFVVGEPNSGMALMVEFLRTKKKHPAVITYMANIALADLLSVIPEPLKI		132
Qy	134	AHYIHNNMTIYGEALCNVLIGFPYGMNTCSILPMPTCSVQRYWYVNPNGHSRKKANINAI		199
Db	133	AHYIHNNMTIYGEALCNVLIGFPYGMNTCSILPMPTCSVQRYWYVNPNGHSRKKANINAI		197
Qy	194	GISLAIWMLILLVTTIPLVYVKQTIFIPALNITTTCHDVLPEQILLVDGMENYFLSLAIGVFL		253
Db	193	GISLAIWMLILLVTTIPLVYVKQTIFIPALNITTTCHDVLPEQILLVDGMENYFLSLAIGVFL		252
Qy	254	PPAFPLTASAVYIMIRMLSSANDENSEKKRRRAIKLITYTAAFTLICPTPENLLVHYHF		313
Db	253	PPAFPLTASAVYIMIRMLSSANDENSEKKRRRAIKLITYTAAFTLICPTPENLLVHYHF		312

PR	09-APR-2003; 2003US-0461323P.
XX	(PRIM-) PRIMAL INC.
XX	Gaitanaris GA, Bergmann JE, Gragorov A, Hohmann J, Li P,
P1	Madsen L, McLwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX	WPI; 2004-390329/36.
DR	N-Psdb; ADO29874.
XX	
PT	Novel mammalian G protein coupled receptors, useful for identifying
PT	compounds that modulates diagnosing and treating disease condition
PT	associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT	pectoris, Parkinson's disease.
PS	Claim 151; SEQ ID NO 412; 542pp; English.
XX	
CC	The invention relates to human and mouse G protein-coupled receptors
CC	(GPCRs) and nucleic acids encoding them. The invention also relates to
CC	sequences at least 90% identical to the GPCR proteins and nucleic acids
CC	of the invention; methods of treating, preventing or diagnosing diseases
CC	associated with GPCRs of the invention; methods of screening for
CC	compounds useful in the treatment of GPCR-related diseases; a transgenic
CC	mouse comprising a GPCR gene of the invention; a mouse comprising a
CC	mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC	from the transgenic mice; kits comprising several mice, each of which has
CC	a mutation in a different GPCR gene of the invention; and kits comprising
CC	probes which hybridize to GPCR polynucleotides of the invention. The
CC	invention further discloses variants of the GPCR polypeptides and vectors
CC	comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC	be used in the diagnosis, treatment or prevention of a wide variety of
CC	diseases including neurological disorders (e.g., Alzheimer's disease,
CC	depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC	disorders of the adrenal gland; disorders of the colon or intestine
CC	(e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC	syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC	myocardial infarction); muscular disorders; blood disorders (e.g.,
CC	anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC	AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC	arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC	obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC	diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC	uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC	thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC	invention. Note: The full sequence data for this patent did not form part
CC	of the printed specification; those sequences not shown were obtained in
CC	electronic format directly from WIPO at
CC	ftp.wipo.int/pub/published_pct_sequences.
XX	
SQ	Sequence 397 AA;
Query Match	93.7%; Score 1903; DB 8; Length 397;
Best Local Similarity	96.9%; Pred. No. 2.9e-196;
Matches 573; Conservative	4; Mismatches 19; Indels 4; Gaps 1
18	SVMTLVPLSTCT-----GTRSSKGRSLIGKVDTSHVTKGVTVETVFSYDERASATLTKG 73
DB	:::::
13	AIILAASISCSGTIGITWRSSSKGRSLIGKVDTSHVTKGVTVETVFSYDERASATLTKG 72
QY	LTTFVLPIVTYTVFVVGGLPSNGMALMVFLEFRKKGHPAVIYMANIALADLSIVMEPLKI 133
DB	LTTTVELPIVTYTVFVVGGLPSNGMALMVFLEFRKKGHPAVIYMANIALADLSIVMEPLKI 132
QY	AVHIGNNMITYEALCNVLIIGFYGNMYCILLFMCLTSQRVMVIVNPGHSKRKANIAI 193
DB	AHHIGNNMITYEALCNVLIIGFYGNMYCILLFMCLTSQRVMVIVNPGHSKRKANIAI 192
QY	GISLAIWLLILVTLPIPLYVKQTIFIPALNITTCDDVLPBEOULLVGDMMFYFLSIAIGVL 253
DB	GISLAIWLLILVTLPIPLYVKQTIFIPALNITTCDDVLPBEOULLVGDMMFYFLSIAIGVL 252
QY	PPAFLTAGSYVLMIRLRSSANDENSEKKRAIKLIVTLAMYLICTPSPNILLVVHYF 313

QY	DB	Sequence	Score	DB	Length	Matches	Mismatches	Indels	Gaps
QY	253	PPAPFLTASAVYLMTRMLRSSAMDENSEKKRKRAKLIYTVLMTLICPTPSNLLVHYHF	93.7%	DB 8	397	373	4	4	1
QY	314	LKSGGSHVVALYIVALCSTLNSCIDPFYFVSHDFRDHAKNALLCRSVRTVKQMOV	96.9%	Pred. No. 2.9e-16;					
DB	313	LKSGGSHVVALYIVALCSTLNSCIDPFYFVSHDFRDHAKNALLCRSVRTVKQMOV							
QY	374	SLTSKSHSRKSSSYSSSTVYKTSY			398				
DB	373	SLTSKSHSRKSSSYSSSTVYKTSY			397				
RESULT 8									
ADST74020	ID	ADST74020 standard; protein; 397 AA.							
AC	ADST74020;								
XX	16-DEC-2004	(first entry)							
XX	Human G-protein coupled proteinase activated receptor 2 (PAR2).								
DE	Human: proteinase activated receptor 2; PAR2; G-protein coupled receptor;								
XX	receptor; cardiac; neuroprotective; nephrotropic; respiratory-gen.;								
KM	gastrointestinal-gen.; gene therapy.								
XX	Homo sapiens.								
OS	MO2004080373-A2.								
XX	23-SEP-2004.								
PD	26-FEB-2004; 2004WO-EP001896.								
XX	11-MAR-2003; 2003EP-00004980.								
XX	(FARB) BAYER HEALTHCARE AG.								
PA	Golz S, Brueggemeier U, Summer H;								
XX	WPI; 2004-677358/66.								
DR	N-PSDB; ADST74019.								
XX	Screening for therapeutic agents for treating e.g., cardiovascular								
PT	diseases by contacting a test compound with a proteinase activated								
PR	receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of								
PT	the test compound.								
XX	Disclosure; SEQ ID NO 2; 121bp; English.								
PS	The present sequence is that of human G-protein coupled proteinase								
XX	activated receptor 2 (PAR2). PAR2 is an antiinflammatory receptor in the								
CC	colon and may also play a role in the airway, regulating sodium ion								
CC	absorption and anion secretion. The invention relates to novel disease								
CC	associations of PAR2 polypeptides and polynucleotides. It also relates to								
CC	novel methods of screening for therapeutic agents for the treatment of								
CC	cardiovascular disorders, gastrointestinal and liver diseases,								
CC	neurological disorders, urological disorders, hematological diseases and								
CC	respiratory diseases in a mammal. Suitable therapeutic agents include a								
CC	small molecule, an RNA molecule, an antisense oligonucleotide, a								
CC	polypeptide, an antibody or a ribozyme. The invention also provides								
CC	pharmaceutical compositions for the treatment of diseases and disorders								
CC	associated with PAR2 comprising a PAR2 polypeptide, PAR2 polynucleotide								
CC	or a regulator or modulator of PAR2 activity. Methods of diagnosing these								
CC	diseases and disorders involve determining the amount of PAR2								
CC	polynucleotide in a sample.								
XX	Sequence 397 AA;								
QY	Query Match	93.7%; Score 1903; DB 8; Length 397;							
Match	Best Local Similarity	96.9%; Pred. No. 2.9e-16;							
Matches	373; Conservative	4; Mismatches 4; Indels 4; Gaps 1;							

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Db      13 AIIAASLSCSGTIGTNRSSKGRSLGKVDGSHYTGKVTETVPSVDFSAVLTKG 72
Qy      74 LTTVFLPIVYTVTVVGVGLPSNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 133
Db      73 LTTVFLPIVYTVTVVGVGLPSNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 132
Qy      134 AYHIGNNMTYGRALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 193
Db      133 AYHIGNNMTYGRALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 192
Qy      194 GISLAIWLLILVLTIPLYVVKQTIFIPALNITTCCHDVLPEQLVGMDFNYFLSLAIGVFL 253
Db      193 GISLAIWLLILVLTIPLYVVKQTIFIPALNITTCCHDVLPEQLVGMDFNYFLSLAIGVFL 252
Qy      254 PPAFLTASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 313
Db      253 PPAFLTASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 312
Qy      314 LKSGQSHVYALYIVALCISTLNSCIDPFIYVFSHDFRDHAKNALCGRSVTVKQMOV 373
Db      313 LKSGQSHVYALYIVALCISTLNSCIDPFIYVFSHDFRDHAKNALCGRSVTVKQMOV 372
Qy      374 SLTSKGRSKSSSYSSSSTTVTKTSY 398
Db      373 SLTSKGRSKSSSYSSSSTTVTKTSY 397

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RESULT 9
ADL61221
ID      ADL61221 standard; protein; 397 AA.
XX
XX      ADL61221;
XX
XX      03-JUN-2004 (first entry)
XX
XX      Human coagulation factor II (thrombin) receptor-like 1 protein.
XX
XX      predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
XX      vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer;
XX      hypervascular disease; angiogenesis; wound healing scar; human;
XX      biomarker; coagulation factor II receptor-like 1; thrombin; receptor.
XX
XX      Homo sapiens.
XX
XX      MO2004020583-A2.
XX
XX      11-MAR-2004.
XX
XX      26-AUG-2003; 2003MO-US026491.
XX
XX      27-AUG-2002; 2002US-0406385P.
XX
XX      (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX      Huang F, Han X, Reeves KA, Anler L, Fairchild CR, Lee FY,
XX      Shaw P;
XX
XX      WPI; 2004-239171/22.
XX      N-PSDB; ADL61084.
XX
XX      New predictor sets with a plurality of polymucleotides and/or
XX      polypeptides whose expression pattern predicts cell response to a
XX      compound that modulates protein tyrosine kinase activity, useful in
XX      treating breast cancer.
XX
XX      Claim 9; SEQ ID NO 145; 649pp; English.
XX
XX      The invention relates to a novel predictor set comprising a plurality of
XX      polymucleotides and/or polypeptides whose expression pattern is
XX      predictive of the response of cells to treatment with a compound that
XX      modulates protein tyrosine kinase activity or members of the protein
XX      tyrosine kinase pathway. The molecules of the invention demonstrate

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CC cytosolic, antiangiogenic, vasotropic and vulnerary activities and may
 CC be useful in the field of pharmacogenomics, in particular for determining
 CC drug sensitivity and in treating breast cancer, hypervascular diseases,
 CC angiogenesis and scars in wound healing. The current sequence is that of
 CC a human protein tyrosine kinase biomarker protein of the invention.

SO Sequence 397 AA;

Query Match 93.5%; Score 1898; DB 8; Length 397;
 Best Local Similarity 96.6%; Pred. No. 9.9e-196;
 Matches 372; Conservative 5; Mismatches 4; Gaps 1;

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Qy      18 SVMTVFLSCT---GTRSSKGRSLGKVDGSHYTGKVTETVPSVDFSAVLTKG 73
Db      13 AIIAASLSCSGTIGTNRSSKGRSLGKVDGSHYTGKVTETVPSVDFSAVLTKG 72
Qy      74 LTTVFLPIVYTVTVVGVGLPSNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 133
Db      73 LTTVFLPIVYTVTVVGVGLPSNGMALWFLPRTKKGGPAVIYMANLADLLSVIWPPLKI 132
Qy      134 AYHIGNNMTYGRALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 193
Db      133 AYHIGNNMTYGRALCNVLI GFPGNNYCSILFMTCISVORVWYVYVPMGHSRKKANIAI 192
Qy      194 GISLAIWLLILVLTIPLYVVKQTIFIPALNITTCCHDVLPEQLVGMDFNYFLSLAIGVFL 253
Db      193 GISLAIWLLILVLTIPLYVVKQTIFIPALNITTCCHDVLPEQLVGMDFNYFLSLAIGVFL 252
Qy      254 PPAFLTASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 313
Db      253 PPAFLTASAYVLMIRMLRSSAMDENSEKKRAIKLIVTLAMYLICFTPSNLLLVHYHF 312
Qy      314 LKSGQSHVYALYIVALCISTLNSCIDPFIYVFSHDFRDHAKNALCGRSVTVKQMOV 373
Db      313 LKSGQSHVYALYIVALCISTLNSCIDPFIYVFSHDFRDHAKNALCGRSVTVKQMOV 372
Qy      374 SLTSKGRSKSSSYSSSSTTVTKTSY 398
Db      373 SLTSKGRSKSSSYSSSSTTVTKTSY 397

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RESULT 10
ABP81907
ID      ABP81907 standard; protein; 397 AA.
XX
XX      ABP81907;
XX
XX      04-MAR-2003 (first entry)
XX
XX      Human proteinase-activated receptor 2 protein SEQ ID NO:300.
XX
XX      G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
XX      G protein-coupled receptor modulator; antibody; immune-related disease;
XX      growth-related disease; cell regeneration-related disease; AIDS; cancer;
XX      immunological-related cell proliferative disease; autoimmune disease;
XX      Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
XX      osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
XX      graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
XX      psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
XX      mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
XX      hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX      ulcer.
XX
XX      Homo sapiens.
XX
XX      MO200261087-A2.
XX
XX      08-AUG-2002.
XX
XX      19-DEC-2001; 2001MO-US050107.
XX      19-DEC-2000; 2000US-0257144P.
XX

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QY 314 LKSGGSHVYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 373
 DB 313 LKSGGSHVYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 372
 QY 374 SLTSKSKSRKSSSYSSSSTTVKTSY 398
 DB 373 PLTSKSKSRKSSSYSSSSTTVKTSY 397

RESULT 15
 AAM01955
 ID AAM01955 standard; protein; 397 AA.
 AC AAM01955;
 DT 02-APR-1997 (first entry)
 DE Human C140 receptor.
 XX C140 receptor; G-protein linked; coupled; seven pass; agonist;
 KM antagonist; hypertension; hypotension; blood pressure.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27 /note= "the signal peptide differs from that encoded by a
 FT genomic DNA sequence for this receptor (see AAM01953),
 FT the signal sequence given here is believed to be the
 FT correct sequence"
 FT Protein 28..397 /note= "mature protein"
 XX
 PN W09623225-A1.
 PD 01-AUG-1996.
 XX
 PD 25-JAN-1996; 96MO-US001179.
 XX
 PR 25-JAN-1995; 95US-00390301.
 XX
 PA (COR-) COR THERAPEUTICS INC.
 XX
 PI Sundelin J, Scarborough RM;
 XX
 DR WPI; 1996-362813/36.
 DR N-PSDB; AAT32039.
 XX
 PT Vector for expression C140 cell surface receptor in host cell - useful to
 PT identify C140 agonist and antagonists, which are antihypertensives and
 PT elevators of blood pressure, respectively.
 XX
 PS Example 5; Fig 11A-B; 60pp; English.
 XX
 CC AAM01955 represents the human C140 receptor (C140R). DNA encoding C140R
 CC may be engineered so as to allow the recombinant expression of C140R in a
 CC suitable host cell, i.e. by removing the native expression-control
 CC sequences and replacing them with control sequences operable in the host.
 CC Such a recombinant receptor can be expressed on the surface of oocytes,
 CC this provides a good assay system for identifying agonists/antagonists of
 CC C140R. The C140 receptor is a G-protein linked receptor and a member of
 CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
 CC receptor passes through the cell membrane seven times, producing seven
 CC transmembrane regions within the receptor molecule). The C140 receptor is
 CC involved in controlling blood pressure. C140 antagonists (see AAM01942-
 CC W01951) are useful to inhibit signalling from this receptor, resulting in
 CC an increase in blood pressure and are therefore useful in pharmaceuticals
 CC for the treatment of hypotension (low blood pressure). Conversely
 CC agonists (see AAM01914-W01941) of C140 are useful in pharmaceuticals for
 CC the treatment of hypertension (high blood pressure)
 CC
 CC Sequence 397 AA,
 SQ

Query Match 92.4%; Score 1872; DB 2; Length 397;
 Best Local Similarity 95.3%; Pred. No. 6.3e-193;
 Matches 367; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

QY 18 SVMTLVFLSCT---GTRSSKGRSLIGKVDGTSHTGKGVTVTVSVDPSASVLTGK 73
 DB :::::|||||
 13 AILMAASLSCSGRTIGTRSSKGRSLIGKVDGTSHTGKGVTVTVSVDPSASVLTGK 72
 QY LTTVFLPIVYTVIVFAVGLPSNGMALWFLPRTKKQHPAVIYMANLADLLSVTFPLKI 133
 DB LTTVFLPIVYTVIVFAVGLPSNGMALWFLPRTKKQHPAVIYMANLADLLSVTFPLKI 132
 QY 134 AYHIGNNWYIGBALCNVLIIGPFYGNMYCSILFWTCISVORVYVIYVPMGHSRKKANIAI 193
 DB 133 AYHIGNNWYIGBALCNVLIIGPFYRNMYCSILFWTCISVORVYVIYVPMGHSRKKANIAI 192
 QY 194 GISLAIWLLTLVTLPIVYVKOTIFIPALNITTCBDVLPGQLVGMFNYFLSLAIGVFL 253
 DB 193 GISLAIWLLTLVTLPIVYVKOTIFIPALNITTCBDVLPGQLVGMFNYFLSLAIGVFL 252
 QY 254 PPAFLTASAYVLMIRMLRSSAMDENSEKKRRAIKLIYTVLAWLIGFTSNLLLVHYF 313
 DB 253 PPAFLTASAYVLMIRMLRSSAMDENSEKKRRAIKLIYTVLAWLIGFTSNLLLVHYF 312
 QY 314 LKSGGSHVYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 373
 DB 313 LKSGGSHVYALYVALCLSTLNSCIDPFVYVFSHPDPAKALLCRSVRTVKOMOV 372
 QY 374 SLTSKSKSRKSSSYSSSSTTVKTSY 398
 DB 373 PLTSKSKSRKSSSYSSSSTTVKTSY 397

Search completed: March 18, 2005, 21:06:43
 Job time: 73.0868 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 21, 2005, 12:11:20 / Search time 825.407 Seconds
(without alignments)
10141.072 Million cell updates/sec

Title: US-10-643-627-62

Perfect score: 1414
Sequence: 1 caaagatgtaacagact.....acaattccacataaagc 1414

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1980s:*
3: geneseqn2000s:*
4: geneseqn2001s:*
5: geneseqn2001s:*
6: geneseqn2002s:*
7: geneseqn2002s:*
8: geneseqn2003s:*
9: geneseqn2003s:*
10: geneseqn2003s:*
11: geneseqn2003s:*
12: geneseqn2004s:*
13: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1414	100.0	1414	2	AA084560 Human C14
2	1414	100.0	1414	2	AA132039 Human C14
3	1279.4	90.5	2876	12	AD028660 Human PAR
4	1273	90.0	1451	3	AA060319 Human PAR
5	1273	90.0	1451	8	AB242755 Human pro
6	1273	90.0	1451	10	ADK52593 Hematolog
7	1273	90.0	1451	11	ADN39780 Cancer/an
8	1273	90.0	1451	13	ADR46617 Cancer-as
9	1273	90.0	1451	13	ADR74019 Human G-P
10	1263.6	89.4	2848	6	AB235045 Human gen
11	1188.4	84.0	8624	6	AA044437 Human coa
12	1182.8	83.6	1194	6	AA044438 Human coa
13	1182.8	83.6	1289	3	AA250773 Human pro
14	1179.6	83.4	1194	12	AD029874 Human GPC
15	1105.8	78.2	1255	2	AA084558 Human C14
16	1105.8	78.2	1255	2	AA132037 Human C14
17	1055.2	74.6	1068	12	AD128650 Human mod
18	1013.2	71.7	963	12	AD128651 Human mod
19	951.8	67.3	963	12	AD128652 Human mod
20	833.8	59.0	2713	9	AC085274 Delayed h

21	833.8	59.0	2732	2	AA084559	AA084559 Murine C1
22	833.8	59.0	2732	2	AA132038	AA132038 Murine C1
23	829.2	58.6	1200	12	AD030165	AD030165 Mouse GPC
24	817.8	57.8	1428	10	AB142343	AB142343 Toxicity
25	805.4	57.0	1477	2	AA084557	AA084557 Murine C1
26	803.8	56.8	1477	2	AA132036	AA132036 Murine C1
27	383	27.1	486	6	ABK55138	ABK55138 Human col
28	303.2	21.4	493	6	ABK27602	ABK27602 Human col
29	303.2	21.4	641	6	AB137070	AB137070 Human col
30	166.4	11.8	3418	10	AB141875	AB141875 Toxicity
31	160.6	11.4	1116	6	ABK70888	ABK70888 Human CDN
32	160.6	11.4	1209	6	ABK70887	ABK70887 Human CDN
33	160.6	11.4	1278	6	ABK70889	ABK70889 Human CDN
34	160.6	11.4	3590	13	ACN38232	ACN38232 Tumour-as
35	156.6	11.1	6203	10	ADG89941	ADG89941 Human coa
36	155.8	11.0	1278	10	ADG89942	ADG89942 Human coa
37	155.8	11.0	1278	12	AD029873	AD029873 Human GPC
38	155.8	11.0	1764	2	AA073590	AA073590 Fragment
39	155.8	11.0	2910	2	AA162461	AA162461 TIR-GPA1
40	155.8	11.0	2910	2	AA162461	AA162461 TIR-GPA1
41	155.8	11.0	3182	3	AA153310	AA153310 Human ade
42	155.8	11.0	3182	3	AA153310	AA153310 Human low
43	155.8	11.0	3182	10	AB297126	AB297126 Human nuc
44	155.8	11.0	3182	11	ABD20575	ABD20575 Human pul
45	155.8	11.0	3472	9	ADA24508	ADA24508 Human CDN
				2	AA232191	AA232191 Human thr

ALIGNMENTS

RESULT 1	AA084560	AA084560 standard; cDNA; 1414 BP.
ID	AA084560	AA084560 standard; cDNA; 1414 BP.
AC	AA084560	
AC	AA084560	
DT	25-MAR-2003	(revised)
DT	22-AUG-1995	(first entry)
XX	Human C140 receptor cDNA.	
XX	G-protein-coupled receptor; G-protein; C140 receptor; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	CDS	50..1243
FT		/*tag= a
XX	MO9503318-A1.	
XX	02-FEB-1995.	
XX	26-JUL-1994;	94MO-US008536.
XX	26-JUL-1993;	93US-00097938.
XX	(CORT-) COR THERAPEUTICS.	
XX	Scarborough RM, Sundelin J;	
XX	WPI; 1995-075182/10.	
DR	P-PSDB; AAR66923.	
XX	New DNA encoding recombinant C140 receptor - and novel agonists and	
PT	antagonists and specific antibodies with therapeutic and diagnostic	
PT	applications.	
XX	Claim 1; Fig 11; 57pp; English.	
PS	A human intestinal tumour cDNA library was subjected to PCR using primers	
XX	designed from the genomic clone (see AA084558) and the amplified fragment	
CC	was cloned in pSG5 and sequenced. There are four AA differences between	

CC the cDNA encoded sequence and that encoded by the genomic DNA. The
 CC genomic DNA sequence and deduced AA sequence are given in AA084560 &
 CC AAR6923. (Updated on 25-MAR-2003 to correct PN field.)
 XX

Sequence 1414 BP; 335 A; 361 C; 309 G; 409 T; 0 U; 0 Other;

Query Match 100.0%; Score 1414; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 CAAAGATTGTATAGACTACTATATAGGCGGAATTCGATCCAGAGAGATGGAGCCCC 60
DB 1 CAAAGATTGTATAGACTACTATATAGGCGGAATTCGATCCAGAGAGATGGAGCCCC 60
QY 61 CAGCGGCGCTGCTGCTGGGGGCGCCGCTCTGCTAGCAGCCCTCTCTCTCTGCAATGG 120
DB 61 CAGCGGCGCTGCTGCTGGGGGCGCCGCTCTGCTAGCAGCCCTCTCTCTCTGCAATGG 120
QY 121 CACCATCCAGAGAACCAATAGATCTCTTAAAGAGAGAGCCCTTATGGTAAAGTTGA 180
DB 121 CACCATCCAGAGAACCAATAGATCTCTTAAAGAGAGAGCCCTTATGGTAAAGTTGA 180
QY 181 CACATCCCAAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 CACATCCCAAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 TTCATGATCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 241 TTCATGATCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 TGTGTTGCGGTGGGTTTGGCAAGTAAAGGCAATGAGCCCTTATGGGTTCTTTTCCG 360
DB 301 TGTGTTGCGGTGGGTTTGGCAAGTAAAGGCAATGAGCCCTTATGGGTTCTTTTCCG 360
QY 361 TAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 TAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 TGTGATCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 TGTGATCTGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 GGAAGCTCTTTGTAATGAGTAAATGAGCTTTTCTATGCAACATGATGTTCCATTC 540
DB 481 GGAAGCTCTTTGTAATGAGTAAATGAGCTTTTCTATGCAACATGATGTTCCATTC 540
QY 541 CTTGATGACCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
DB 541 CTTGATGACCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 CAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 CAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 GGTGACATCCCTTTGTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 GGTGACATCCCTTTGTATGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 GACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
DB 721 GACCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
QY 781 CTCTGAGCATTGGGGTCTTTCTGTTCCAGGCTTCTCAAGAGCTCTGCTATGAGCT 840
DB 781 CTCTGAGCATTGGGGTCTTTCTGTTCCAGGCTTCTCAAGAGCTCTGCTATGAGCT 840
QY 841 GATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
DB 841 GATGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
QY 901 GGGCATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 GGGCATCAAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960

```

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QY 961 CTTTCTGCTGTTGAGTCAATTAATTTCTGATTAAGAGCCAGGGCCAGAGCATTCTATGC 1020
DB 961 CTTTCTGCTGTTGAGTCAATTAATTTCTGATTAAGAGCCAGGGCCAGAGCATTCTATGC 1020
QY 1021 CTTGATCATTGTAAGCTCTGCTCTCTGCTCTCTTAAAGAGAGAGAGAGAGAGAG 1080
DB 1021 CTTGATCATTGTAAGCTCTGCTCTCTGCTCTCTTAAAGAGAGAGAGAGAGAGAG 1080
QY 1081 TTACTTGTGTTCAATGATTTTCAAGAGAGATGATGATGATGATGATGATGATGAT 1140
DB 1081 TTACTTGTGTTCAATGATTTTCAAGAGAGATGATGATGATGATGATGATGATGAT 1140
QY 1141 CCGGACTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
DB 1141 CCGGACTGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
QY 1201 CTCTTACTCTTCAAGTTCAACAAGTCTGTTAAGAGAGAGAGAGAGAGAGAGAGAG 1260
DB 1201 CTCTTACTCTTCAAGTTCAACAAGTCTGTTAAGAGAGAGAGAGAGAGAGAGAGAG 1260
QY 1261 ATGGGAATTGCAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
DB 1261 ATGGGAATTGCAAGTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
QY 1321 TCCGATCCAGATCTTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB 1321 TCCGATCCAGATCTTATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 1381 AAGCAATGCAATCACAATTTTCAACAATTAAGC 1414
DB 1381 AAGCAATGCAATCACAATTTTCAACAATTAAGC 1414

```

RESULT 2

AAT32039 standard; cDNA, 1414 BP.

AAT32039;

02-APR-1997 (first entry)

Human C140 receptor cDNA clone.

C140 receptor; G-protein linked; coupled; seven pass; agonist;

antagonist; hypertension; hypotension; blood pressure; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 50..1243

sig_peptide 50..130

mat_peptide 131..1240

W09623225-A1.

01-AUG-1996.

25-JAN-1996; 96WO-US001179.

25-JAN-1995; 95US-00390301.

(COR-) COR THERAPEUTICS INC.

Sundelin J, Scarborough RM;

XX WP1, 1996-362813/36.
DR P-PSDB, AAW01955.

PT Vector for expression C140 cell surface receptor in host cell - useful to
PT identify C140 agonist and antagonists, which are antihypertensives and
XX elevators of blood pressure, respectively.

PS Example 5, Fig 11A-B, 60pp, English.

XX AAT303 encodes the human C140 receptor (C140R). The sequence may be
CC engineered so as to allow the recombinant expression of C140R in a
CC suitable host cell, i.e. by removing the native expression-control
CC sequence and replacing them with control sequences operable in the host.
CC Such a recombinant receptor can be expressed on the surface of oocytes,
CC this provides a good assay system for identifying agonists/antagonists of
CC the C140 receptor. The C140 receptor is a G-protein linked receptor and a member of
CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
CC transmembrane regions within the cell membrane seven times, producing seven
CC transmembrane regions within the receptor molecule). The C140 receptor is
CC involved in controlling blood pressure. C140 antagonists (see AAW01942-
CC W01951) are useful to inhibit signalling from this receptor, resulting in
CC an increase in blood pressure and are therefore useful in pharmaceuticals
CC for the treatment of hypertension (low blood pressure). Conversely
CC agonists (see AAW01914- AAW01941) of C140 are useful in pharmaceuticals
CC for the treatment of hypertension (high blood pressure)

XX Sequence 1414 BP, 335 A, 361 C, 309 G, 409 T, 0 U, 0 Other;

Query Match 100.0%; Score 1414; DB 2; Length 1414;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAAGAATTGTAATGACACTATGAGGGAATTCAGATCCAGAGATGCGAGCCC 60
DB 1 CAAGAATTGTAATGACACTATGAGGGAATTCAGATCCAGAGATGCGAGCCC 60
QY 61 CAGCGGGGGTGGCTGTGGGGGGCCGCACTCTGATGAGAGCCCTCTCTCGAGTGG 120
DB 61 CAGCGGGGGTGGCTGTGGGGGGCCGCACTCTGATGAGAGCCCTCTCTCGAGTGG 120
QY 121 CACCATCCAGAGAACCAATAGATCTCTAAAGAGAGAGCCCTTAATGGATGGATGG 180
DB 121 CACCATCCAGAGAACCAATAGATCTCTAAAGAGAGAGCCCTTAATGGATGGATGG 180
QY 181 CACATCCCACTGACCTGAGAAAGAGATTACATGAAACAGTCTTTCTGTGATGATT 240
DB 181 CACATCCCACTGACCTGAGAAAGAGATTACATGAAACAGTCTTTCTGTGATGATT 240
QY 241 TTTCTGATCTGTCTGCTGGGAAACAGTACCACTGTCTTCTTCAATGTCTACCAAT 300
DB 241 TTTCTGATCTGTCTGCTGGGAAACAGTACCACTGTCTTCTTCAATGTCTACCAAT 300
QY 301 TGTGTTTGGCGTGGTGGTGGCAAGTAAAGGCAATGAGCCCTTAATGGATGGATGG 360
DB 301 TGTGTTTGGCGTGGTGGTGGCAAGTAAAGGCAATGAGCCCTTAATGGATGGATGG 360
QY 361 TAAAGAAAGACACCTGCTGTGATTTACATGSCCAATGTGGCTTGGCTGACCTCTCTC 420
DB 361 TAAAGAAAGACACCTGCTGTGATTTACATGSCCAATGTGGCTTGGCTGACCTCTCTC 420
QY 421 TGTCACTGTGTTCCCTTGAAGATGTCTATACATACATGAGCAACATGGAATTTATGG 480
DB 421 TGTCACTGTGTTCCCTTGAAGATGTCTATACATACATGAGCAACATGGAATTTATGG 480
QY 481 GGAAGCTCTTGTATATGTCTTATTTGCTTTTCTATGCAATGATCTTCAATCTT 540
DB 481 GGAAGCTCTTGTATATGTCTTATTTGCTTTTCTATGCAATGATCTTCAATCTT 540
QY 541 CTTTCATGACCTGCTGATGATGCAAGATTTGGGTATCTGTAACCCCATGGGGCACTC 600
DB 541 CTTTCATGACCTGCTGATGATGCAAGATTTGGGTATCTGTAACCCCATGGGGCACTC 600

QY 601 CAGAGAAAGAGCAAAATTCGCAATGAGCATCTCCCTGGCAATATAGCTGTGACTGTCT 660
DB 601 CAGAGAAAGAGCAAAATTCGCAATGAGCATCTCCCTGGCAATATAGCTGTGACTGTCT 660
QY 661 GGTTCACCATCTTTGTATGTCTGTAAAGACACCATCTTCAATCTCTGCTGAAATCAC 720
DB 661 GGTTCACCATCTTTGTATGTCTGTAAAGACACCATCTTCAATCTCTGCTGAAATCAC 720
QY 721 GACCTGATGATGTTTGTGCTGAGAGAGCTCTGTGGGAGAGATGTTCAATCTTCT 780
DB 721 GACCTGATGATGTTTGTGCTGAGAGAGCTCTGTGGGAGAGATGTTCAATCTTCT 780
QY 781 CTCTGAGCATTTGGGGTCTTTCTGTGTTCCAGGCTTCTCAAGCTCTGCTATGTGCT 840
DB 781 CTCTGAGCATTTGGGGTCTTTCTGTGTTCCAGGCTTCTCAAGCTCTGCTATGTGCT 840
QY 841 GATGATCAGAAATCTGCGATCTTCTGCAATGATGAAACTCAGAGAGAAAGAGAG 900
DB 841 GATGATCAGAAATCTGCGATCTTCTGCAATGATGAAACTCAGAGAGAAAGAGAG 900
QY 901 GGGCATCAAACTGATGTCATCTCTCCGAGCATGTAATGCTTCTCTCACTCTAGTAA 960
DB 901 GGGCATCAAACTGATGTCATCTCTCCGAGCATGTAATGCTTCTCTCACTCTAGTAA 960
QY 961 CTTTCTGCTTGTGTGATTAATTTCTGATTAAGAGCCAGGCGCAGAGCATGTATGC 1020
DB 961 CTTTCTGCTTGTGTGATTAATTTCTGATTAAGAGCCAGGCGCAGAGCATGTATGC 1020
QY 1021 CTTGATCAATTTAGCCCTCTGCTCTCTCACTTAAAGCTGATGAGCCCTTTGTCTA 1080
DB 1021 CTTGATCAATTTAGCCCTCTGCTCTCTCACTTAAAGCTGATGAGCCCTTTGTCTA 1080
QY 1081 TTAATTTGTTTCAATGATTTTCAAGGATCATGAAAGAGCTCTCTTCCGAATGT 1140
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QY 1141 CCGCATCTGTAAGACAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1200
DB 1141 CCGCATCTGTAAGACAGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 1200
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QY 1261 ATGGGAATTCAGAGTATGAGTAACTGTTAATGTTATGAGAGAGCTGTCTGTTATT 1320
DB 1261 ATGGGAATTCAGAGTATGAGTAACTGTTAATGTTATGAGAGAGCTGTCTGTTATT 1320
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DB 1321 TCCGATTCAGATCTTAATTAAGCAGACTGTTTATGAGCTTAATTAATGTTAAT 1380
QY 1381 AAAGCAATGACATCAAAATTTCACAAAATTAAGC 1414
DB 1381 AAAGCAATGACATCAAAATTTCACAAAATTAAGC 1414

RESULT 3

ADO28600
ID ADO28600 standard; cDNA, 2876 BP.

XX ADO28600;

XX 12-AUG-2004 (first entry)

XX Human PAR2 encoding cDNA SEQ ID NO:29.

XX high-grade dysplasia; KID; oesophageal adenocarcinoma;

XX neo-plastic transformation; cancer; cytotoxic; gene therapy; human;

XX PAR2; chromosome 5; gene; ss.

XX Homo sapiens.

```

FH Key Location/Qualifiers
FT CDS 158..1348
FT /tag= a
FT /product= "PAR2"
FT /transl_except= (pos:287..292,aa:Ser)
FT /transl_except= (pos:461..466,aa:Thr)
FT /transl_except= (pos:635..640,aa:Ser)
FT /transl_except= (pos:809..814,aa:Ala)
FT /transl_except= (pos:983..988,aa:Ser)
FT /transl_except= (pos:1157..1162,aa:Asn)
FT /transl_except= (pos:1331..1336,aa:Lys)
XX MO200404178-A2.
XX
XX 27-MAY-2004.
XX
XX 13-NOV-2003; 2003WO-US036260.
XX
XX 13-NOV-2002; 2002US-0425813P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Smith V;
XX
XX WPI, 2004-420319/39.
XX
XX P-PSDB; ADO28601.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample
XX comprises establishing the level of expression in the test tissue sample
XX of the genes.
XX
XX Claim 1; SEQ ID NO 29; 256bp; English.
XX
XX The present invention describes a method for detecting high-grade
XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
XX (1) identifying an oesophageal tissue susceptible to oesophageal
XX adenocarcinoma; (2) determining the predisposition of a mammalian tissue
XX to a neo-plastic transformation by detecting HGD in cells of the tissue;
XX and (3) detecting cancer in a patient. The method can be used in
XX detecting HGD and cancer in cells of a mammalian tissue sample. The
XX methods and compositions of the present invention can be used in treating
XX and preventing HGD and cancer, and in gene therapy. The present sequence
XX encodes human PAR2, which is used in the exemplification of the present
XX invention. The human PAR2 gene is located on chromosome 5.
XX
XX Sequence 2876 BP; 772 A; 632 C; 629 G; 843 T; 0 U; 0 Other;
SQ
Query Match 90.5%; Score 1279.4; DB 12; Length 2876;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1298; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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Db 434 GGCATGCCCCCTGGGTCTTTCTTTCCGAACCTAAGAAAGACACCCCTGTGATTAC 493
Qy 389 ATGGCCAAATCGACCTTGGCTGAACCTCTCTGTGCATGTGGTCCCTTGAAGATTGCC 448
Db 494 ATGGCCAAATCGACCTTGGCTGAACCTCTCTGTGCATGTGGTCCCTTGAAGATTGCC 553
Qy 449 TATCACAATACAGGCAACACTGATTTATGGGAAAGCTCTTTGTAATGTCTTATGGC 508
Db 554 TATCACAATACAGGCAACACTGATTTATGGGAAAGCTCTTTGTAATGTCTTATGGC 613
Qy 509 TTTTCTATCGAACAATGACTGTTCCATTCTCTTCATGACCGGCTCAGTGTGAGAG 568
Db 614 TTTTCTATGGAACAATGACTGTTCCATTCTCTTCATGACCGGCTCAGTGTGAGAG 673
Qy 569 TATGGGTATCGTGAACCCCAATGGGCACTCCAGAAAGGCAAACTTGCATATGCG 628
Db 674 TATGGGTATCGTGAACCCCAATGGGCACTCCAGAAAGGCAAACTTGCATATGCG 733
Qy 629 ATCTCCCTGGCAATATGGCTGCTGACTGTGTGTCAACATCCCTTTGTAATGCTGAAG 688
Db 734 ATCTCCCTGGCAATATGGCTGCTGACTGTGTGTCAACATCCCTTTGTAATGCTGAAG 793
Qy 689 CAGACCATCTTGAATTCCTGCGCCCTGAACATCAGACCTGTGATGATGTTTGCCTGAGC 748
Db 794 CAGACCATCTTGAATTCCTGCGCCCTGAACATCAGACCTGTGATGATGTTTGCCTGAGC 853
Qy 749 CTCTTGTGGGAGACATGTTCAATTACTTCTCTCTCTGCGCATTTGGGGTCTTCTGTT 808
Db 854 CTCTTGTGGGAGACATGTTCAATTACTTCTCTCTCTGCGCATTTGGGGTCTTCTGTT 913
Qy 809 CCAAGCTTCTCAAGACCTCTGCTATGTGTGATGATGATGATGATGATGATGATGATGAT 868
Db 914 CCAAGCTTCTCAAGACCTCTGCTATGTGTGATGATGATGATGATGATGATGATGATGAT 973
Qy 869 ATGGAATGAAGAACCTCAGAGAAAGAAAGAGAGGACATCAATCTCATTTGACTGCTCG 928
Db 974 ATGGAATGAAGAACCTCAGAGAAAGAAAGAGAGGACATCAATCTCATTTGACTGCTCG 1033
Qy 929 GGCATGTACTGTATCTGCTTCACTCTGTAACTCTTCTGCTGTGTGTGTGTGTGTGTGTG 988
Db 1034 GGCATGTACTGTATCTGCTTCACTCTGTAACTCTTCTGCTGTGTGTGTGTGTGTGTGTG 1093
Qy 989 ATTTAAGAGCCAGGCGCAGAGCCATGTCTATGCTTGTGATGATGATGATGATGATGATGAT 1048
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Db 1214 CATGCAAGAACGCTCTCTTGTGCCAAGTGTCCGACATGTAAAGAGATGCAAGTATCC 1273
Qy 1169 CTCACCTCAAAAGAACCTCCAGAAATCGAAGTCTTACTCTTCAAGTTCAACACTGT 1228
Db 1274 CTCACCTCAAAAGAACCTCCAGAAATCGAAGTCTTACTCTTCAAGTTCAACACTGT 1333
Qy 1229 AAGACCTCTATTTGATTTTCAAGGCTCAGATGGGAATTGACAAGTAGTAGAAG 1288
Db 1334 AAGACCTCTATTTGATTTTCAAGGCTCAGATGGGAATTGACAAGTAGTAGAAG 1393
Qy 1289 CTGTTTAATGTATAGAGACGTGTCTGTATTTCCGAGTCCAGATCTTAATTAAGAGAA 1348
Db 1394 CTGTTTAATGTATAGAGACGTGTCTGTATTTCCGAGTCCAGATCTTAATTAAGAGAA 1453
Qy 1349 CTGTTTAT 1357
Db 1454 CATGTGAT 1462

```

RESULT 4
AAC60319

ID AAC60319 standard; DNA; 1451 BP.
 XX AAC60319;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Human PAR-2 DNA.
 XX
 KW PAR-2; protease activated receptor-2; BCL-2; inflammatory disease;
 KM asthma; chronic obstructive pulmonary; arthritis; inflammatory bowel;
 KW psoriasis; eczema; multiple sclerosis; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0200063371-A1.
 XX
 PD 26-OCT-2000.
 XX
 PF 17-APR-2000; 2000MO-GB001455.
 XX
 PR 15-APR-1999; 99GB-00008513.
 XX
 PA (UYSO-) UNIV SOUTHAMPTON.
 XX
 PI Wallis AF, Palmer K, Compton SJ, Cairns JA, Gough AC;
 XX WPI, 2000-679599/66.
 XX
 DR
 XX
 PT Protease activated receptor 2 variants useful for treating inflammatory
 PT diseases such as asthma, arthritis and psoriasis, and as hypertensives,
 PT has reduced sensitivity to trypsin.
 XX
 PS Disclosure; Page 54-55; 59pp; English.
 XX
 CC The present invention relates to a variant protease activated receptor 2
 CC (PAR-2). The invention is useful for identifying an individual having a
 CC polymorphism in the BCL-2 region of one or both PAR-2 gene alleles. The
 CC invention may be used to develop treatments for inflammatory diseases
 CC such as asthma, chronic obstructive pulmonary diseases, arthritis,
 CC inflammatory bowel diseases, psoriasis and eczema, multiple sclerosis and
 CC to raise blood pressure
 CC
 SQ Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;
 Query Match 90.0%; Score 1273; DB 3; Length 1451;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 29 GGGGAATTGGGATCCAGAGAGATGCGAGCCCGGCGGCGTGGGGGCGCC 88
 DB 127 GGGGTCGGGCTTCAGAGAGATGCGAGCCCGGCGGCGTGGGGGCGCC 186
 QY 89 ATCTGTGACAGCTCTCTCTCTGAGTGGCACTCCAGAGAACCAATAGTCTCT 148
 DB 187 ATCTGTGACAGCTCTCTCTCTGAGTGGCACTCCAGAGAACCAATAGTCTCT 246
 QY 149 AAGGAAGAGCTTATGTGTAAGTGAATGCGACATCCACGTCACCTGAGAAAGATT 208
 DB 247 AAGGAAGAGCTTATGTGTAAGTGAATGCGACATCCACGTCACCTGAGAAAGATT 306
 QY 209 ACAGTTGAACAGCTTTTCTGAGATGAGTTTCTGATCTGCTGCGGAGAACTG 268
 DB 307 ACAGTTGAACAGCTTTTCTGAGATGAGTTTCTGATCTGCTGCGGAGAACTG 366
 QY 269 ACCAGTGTCTTCTTCCATTTGTCTACACATTTGTTGGGTGGTTGCCAATGAC 328
 DB 367 ACCAGTGTCTTCTTCCATTTGTCTACACATTTGTTGGGTGGTTGCCAATGAC 426
 QY 329 GGCATGGCCCTTAATGGGTCTTTCTTTCCGAATGAAGAAAGACCTGCTGTGATTAC 388
 DB 427 GGCATGGCCCTTAATGGGTCTTTCTTTCCGAATGAAGAAAGACCTGCTGTGATTAC 486
 QY 389 ATGGCCAAATCTGGGCTTGGGTGACCTCTCTGTCTATCTGGTTCCCTTGAAGATTGCC 448

DB 487 ATGGCCAAATCTGGGCTTGGGTGACCTCTCTGTCTATCTGGTTCCCTTGAAGATTGCC 546
 QY 449 TATCACTAATAGGCAACACTGATTTATGAGGAAGCTTTGTATATGCTTATTGGC 508
 DB 547 TATCACTAATAGGCAACACTGATTTATGAGGAAGCTTTGTATATGCTTATTGGC 606
 QY 509 TTTTCTAATGCAACATGATCTGTCTCAATCTCTTCAATGACCTGCTCAGTGTGACAGG 568
 DB 607 TTTTCTAATGCAACATGATCTGTCTCAATCTCTTCAATGACCTGCTCAGTGTGACAGG 666
 QY 569 TATTGGTCAATGTAACCCCATGGGCACTCCAGAGAAAGGCAACATTGCCATTGGC 628
 DB 667 TATTGGTCAATGTAACCCCATGGGCACTCCAGAGAAAGGCAACATTGCCATTGGC 726
 QY 629 ATCTCCCTGGCAATATGAGCTGTGACCTGTGCTGTGATCACTCCCTTGTATATGCTGAG 688
 DB 727 ATCTCCCTGGCAATATGAGCTGTGATTTGCTGTGATCACTCCCTTGTATATGCTGAG 786
 QY 689 CAGACATCTTCAATTCCTGCTGAAATGATGACAGACCTGATGATGTTTGGCTGAGCAG 748
 DB 787 CAGACATCTTCAATTCCTGCTGAAATGATGACAGACCTGATGATGTTTGGCTGAGCAG 846
 QY 749 CTCTGGTGGAGACATGTTCAATTAATCTCTCTGCGCAATGGGATCTTCTGTTTC 808
 DB 847 CTCTGGTGGAGACATGTTCAATTAATCTCTCTGCGCAATGGGATCTTCTGTTTC 906
 QY 809 CAGACCTTCTCAAGCTCTGCTGTATGCTGTATGATGATGATGCTGCAATCTTCTGCC 868
 DB 907 CAGACCTTCTCAAGCTCTGCTGTATGCTGTATGATGATGATGCTGCAATCTTCTGCC 966
 QY 869 ATGATGAACATCAGAGAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 928
 DB 967 ATGATGAACATCAGAGAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1026
 QY 929 GGCATGACCTGATGCTGCTTCACTCTGATGACCTTCTGCTGCTGCTGCTGCTGCTGCTG 988
 DB 1027 GGCATGACCTGATGCTGCTTCACTCTGATGACCTTCTGCTGCTGCTGCTGCTGCTGCTG 1086
 QY 989 ATTAAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1048
 DB 1087 ATTAAGAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1146
 QY 1049 ACCCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1108
 DB 1147 ACCCTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1206
 QY 1109 CATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1168
 DB 1207 CATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1266
 QY 1169 CTGACCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1228
 DB 1267 CTGACCTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1326
 QY 1229 AAGAGCTCCATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1288
 DB 1327 AAGAGCTCCATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1386
 QY 1289 CTGTTTAATGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1348
 DB 1387 CTGTTTAATGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1446
 QY 1349 C 1349
 DB 1447 C 1447
 RESULT 5
 ID AB242755 standard; DNA; 1451 BP.
 XX
 AC AB242755;

XX 04-MAR-2003 (first entry)
DB Human proteinase-activated receptor 2 nucleotide seq ID NO:299.
XX
KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related disease; cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KM osteoporosis; cardiovascular; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer; gene; db.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burnier GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
XX
PT P-PSDB; ABP81907.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PT Disclosure; Fig 1; 523dp; English.
XX
PS The present invention describes antigenic peptides (I) comprising: (a)
XX any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
XX acids. Also described: (1) an assay for the detection of a particular G
XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
XX and (2) an isolated antibody having high specificity and high affinity or
XX avidity for a particular GPCR. (I) can be used as GPCR modulators and in
XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
XX antibody against a particular GPCR, and in the production of specific
XX antibodies. The peptides and antibodies are also useful for detecting the
XX presence or absence of corresponding GPCRs. The antigenic peptides for
XX GPCRs and antibodies are useful for diagnosing and designing drugs for
XX treating immune-related diseases, growth-related diseases, cell
XX regeneration-related disease, immunological-related cell proliferative
XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
XX any other disorder in which GPCRs are involved. The antibodies may be
XX used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
XX GPCR proteins given in ABP81675 to ABP82018, which are used in the
XX exemplification of the present invention
XX
SQ Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;

Query Match 90.0%; Score 1273; DB 8; Length 1451;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY	29	GGCGAATTGGATCCAGAGGATGCGGAGCCCGGCGCGCTGGTGGGGCGCGCC	88
DB	127	GGCGTCGGGGCTTCCAGAGATGCGGAGCCCGGCGCGCTGGTGGGGCGCGCC	186
QY	89	ATCTGTGACGACCTCTCTCTCTGACGTGGACCATCCAGAAACAATAGATCTCT	148
DB	187	ATCTGTGACGACCTCTCTCTCTGACGTGGACCATCCAGAAACAATAGATCTCT	246
QY	149	AAAGAGAAAGGCTTATGTTAGTTGATGACATCCACGTCACTGAAAGAGATT	208
DB	247	AAAGAGAAAGGCTTATGTTAGTTGATGACATCCACGTCACTGAAAGAGATT	306
QY	209	ACAGTTGAAACAGCTCTTTCTGTGATGATTTCTGACATCTCTCGCTGAAACCTG	268
DB	307	ACAGTTGAAACAGCTCTTTCTGTGATGATTTCTGACATCTCTCGCTGAAACCTG	366
QY	269	ACCAGTCTCTCTCTCAATGTTGTTCAACAATTTGTTGCGGTGGGTTGGCAATGAC	328
DB	367	ACCAGTCTCTCTCTCTCAATGTTGTTCAACAATTTGTTGCGGTGGGTTGGCAATGAC	426
QY	329	GGCATGGCCCTATGAGGCTCTTCTTTCGAACTAAGAAAGACACCTGCTGATTTAC	388
DB	427	GGCATGGCCCTATGAGGCTCTTCTTTCGAACTAAGAAAGACACCTGCTGATTTAC	486
QY	389	ATGGCCATCTGGCTTGGCTGACCTCTCTCTGTCATCTGTTCCCTTGAAGATTGCC	448
DB	487	ATGGCCATCTGGCTTGGCTGACCTCTCTCTGTCATCTGTTCCCTTGAAGATTGCC	546
QY	449	TATCACAATCATGGCAACAACATGATTTATGAGGAAAGCTCTTGTATATGCTTATGCG	508
DB	547	TATCACAATCATGGCAACAACATGATTTATGAGGAAAGCTCTTGTATATGCTTATGCG	606
QY	509	TTTTTCTATGGAACATGATCTGTTCCATCTCTTTCATGACCTGCTCAGTGTGACAGG	568
DB	607	TTTTTCTATGGAACATGATCTGTTCCATCTCTTTCATGACCTGCTCAGTGTGACAGG	666
QY	569	TATTTGGTATATGTGAACCCCATGAGGAGCTCCAGAAAGAAAGCAATTCGATTTGCG	628
DB	667	TATTTGGTATATGTGAACCCCATGAGGAGCTCCAGAAAGAAAGCAATTCGATTTGCG	726
QY	629	ATCTCCCTGGCAATATGAGCTGCTGACTGCTGTCACCATCCCTTGTATGTCGGAAG	688
DB	727	ATCTCCCTGGCAATATGAGCTGCTGACTGCTGTCACCATCCCTTGTATGTCGGAAG	786
QY	689	CAGACCATCTTATCTCTGCTGCTGAAATCATCAGACCTGCTGATGATGTTTGGCTGAGC	748
DB	787	CAGACCATCTTATCTCTGCTGCTGAAATCATCAGACCTGCTGATGATGTTTGGCTGAGC	846
QY	749	CTTTTGTGAGGAGACATGTTCAATTAATCTCTCTCTGAGCCATGAGGCTCTTCTGTTTC	808
DB	847	CTTTTGTGAGGAGACATGTTCAATTAATCTCTCTCTGAGCCATGAGGCTCTTCTGTTTC	906
QY	809	CCAGCTTCTCTCAAGACCTCTGCTATGCTGATGATCAGAAATGCTGATCTTCTGCGC	868
DB	907	CCAGCTTCTCTCAAGACCTCTGCTATGCTGATGATCAGAAATGCTGATCTTCTGCGC	966
QY	869	ATGATGAAATCTCAGAGAAAGAAAGAAAGAGGCGCATCAAACTCATGTCATCTCTG	928
DB	967	ATGATGAAATCTCAGAGAAAGAAAGAAAGAGGCGCATCAAACTCATGTCATCTCTG	1026
QY	929	GGCATGTACTGATCTGCTTCACTCTGATTAACCTTCTGCTGTGTGTGATTAATTTCTG	988
DB	1027	GGCATGTACTGATCTGCTTCACTCTGATTAACCTTCTGCTGTGTGTGATTAATTTCTG	1086
QY	989	ATTTAAGAGCAGAGGCGCAGAGCCATGTCATGCTGATCAATTTAGCCCTCTGCTCTCT	1048
DB	1087	ATTTAAGAGCAGAGGCGCAGAGCCATGTCATGCTGATCAATTTAGCCCTCTGCTCTCT	1146
QY	1049	ACCTTTAAGAGCTGATGACACCTTTTGTCTATTAATTTGTTTCAATGATTTACAGGAT	1108
DB	1147	ACCTTTAAGAGCTGATGACACCTTTTGTCTATTAATTTGTTTCAATGATTTACAGGAT	1206
QY	1109	CATGCAAGAACGCTCTCTTTCGGAAGTGTCCGACATGTATTAAGACATGCAAGTACCC	1168

Db 1207 CATGCAAGAAAGCGCTCTCTTCGGAAGTCCGACCTGTAAGCAAGATATCC 1266
 Qy 1169 CTCACCTCAAGAAACCTCCAGGAATCCAGCTCTTAAGTTCAACCACTGTT 1228
 Db 1267 CTCACCTCAAGAAACCTCCAGGAATCCAGCTCTTAAGTTCAACCACTGTT 1326
 Qy 1229 AAGACCTCTTATGAGTTTCAGATCTCCAGATGGGAATTGCAAGTGAATGGAGAC 1288
 Db 1327 AAGACCTCTTATGAGTTTCAGATCTCCAGATGGGAATTGCAAGTGAATGGAGAC 1386
 Qy 1289 CTGTTTATGTTATGAGACCTGCTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAAA 1348
 Db 1387 CTGTTTATGTTATGAGACCTGCTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAAA 1446
 Qy 1349 C 1349
 Db 1447 C 1447

RESULT 6
 ADK52593
 ID ADK52593 standard; DNA; 1451 BP.
 AC ADK52593;
 XX 06-MAY-2004 (first entry)
 DT
 DE Hematological disorder associated Gene ID 340.
 XX cytostatic; antianemic; antistickling; virucide; hemostatic; nephrotropic;
 KM cytostatic; thrombolytic; antiparasitic; gene therapy;
 KM hematologic disorder; cancer; Sickle Cell Anemia;
 KM Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;
 KM Reticuloblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;
 KM transfusion reaction; Erythroblastosis; mechanical trauma;
 KM micro-angiopathic hemolytic anemia; parasite infection; gene; ds.
 XX
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 148..1341
 FT /*tag= a
 XX
 PN MO2003065871-A2.
 PD 14-AUG-2003.
 XX 28-JAN-2003; 2003WO-US002484.
 XX 04-FEB-2002; 2002US-0354333P.
 PR 28-FEB-2002; 2002US-0360258P.
 PR 15-MAR-2002; 2002US-0364476P.
 PR 26-APR-2002; 2002US-0375626P.
 PR 06-JUN-2002; 2002US-0386494P.
 PR 24-JUN-2002; 2002US-0390965P.
 PR 28-JUN-2002; 2002US-0392480P.
 PR 03-JUL-2002; 2002US-0394128P.
 PR 31-JUL-2002; 2002US-0399783P.
 PR 13-AUG-2002; 2002US-0403221P.
 PR 30-AUG-2002; 2002US-0407045P.
 PR 25-NOV-2002; 2002US-0429048P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Carrol JM, Healy A, Welch NS, Kelly LM;
 XX WPI; 2003-731464/69.
 DR P-PSDB; ADK52594.
 XX
 PT Identifying a compound capable of treating a hematologic disorder (e.g. PT
 anemia or leukemia) comprises assaying the ability of the compound to
 modulate the expression or activity of e.g. 131,148, 199 or 12303

PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 51; 232bp; English.
 XX
 CC The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprising assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
 CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickle Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC Polycythemia Vera, Lymphoma, Reticuloblastoma, Hemophilia, disorders
 CC associated with an increased risk of thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and
 CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angiopathic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to one of the
 CC genes modulated the compound.
 XX
 SQ Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;
 Query Match 90.0%; Score 1273; DB 10; Length 1451;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 29 GCGGATTCGGAATCCAGAGAGATGCGAGCCCGGCGGCTGCTGGGGGCGGCC 88
 Db 127 GCGGTGCGGGCTTCCAGAGAGATGCGAGCCCGGCGGCTGCTGGGGGCGGCC 186
 Qy 89 ATCTGTACACAGCTCTCTCTCTGATGGGACCATCCAAAGAACATTAATCTCT 148
 Db 187 ATCTGTACACAGCTCTCTCTCTGATGGGACCATCCAAAGAACATTAATCTCT 246
 Qy 149 AAAGAAAGAGCCTTATTTGATGATGACATCCACGTCATGTGAAAAGAGTT 208
 Db 247 AAAGAAAGAGCCTTATTTGATGATGACATCCACGTCATGTGAAAAGAGTT 306
 Qy 209 ACAATTGAAACAGCTTTTCTGTGATGAGTTTCTGATCTGTCTGCTGAAAATCTG 268
 Db 307 ACAATTGAAACAGCTTTTCTGTGATGAGTTTCTGATCTGTCTGCTGAAAATCTG 366
 Qy 269 ACCACTGTCTCTCTGCAATTTGTCACAAATTTGTTCCGGTGGTTGCCAATTAAC 328
 Db 367 ACCACTGTCTCTCTGCAATTTGTCACAAATTTGTTGTTGGGTTGCCAATTAAC 426
 Qy 329 GGCATGGCCTATGAGGCTTTCTTTCCGAACCTAAGAAAGAGACCTGCTGTGATTTAC 388
 Db 427 GGCATGGCCTATGAGGCTTTCTTTCCGAACCTAAGAAAGAGACCTGCTGTGATTTAC 486
 Qy 389 ATGGCAATCTGGGCTTGGCTGACCTCTCTGTCACTGTGTTCCCTTGAAGATTGCC 448
 Db 487 ATGGCAATCTGGGCTTGGCTGACCTCTCTGTCACTGTGTTCCCTTGAAGATTGCC 546
 Qy 449 TATCACTATACATGGCAACAATGATTTATGAGGAAGCTTTGTATATGCTTATGGC 508
 Db 547 TATCACTATACATGGCAACAATGATTTATGAGGAAGCTTTGTATATGCTTATGGC 606
 Qy 509 TTTTCTATGCAACAATGATCTGTCATCTCTTATGACCTGCTCAGTGTGACAGG 568
 Db 607 TTTTCTATGCAACAATGATCTGTCATCTCTTATGACCTGCTCAGTGTGACAGG 666
 Qy 569 TATTTGGTCATGTGAACCCCATGGGCACTCCAGAAAGAGCAACATTTGCCATTGGC 628
 Db 667 TATTTGGTCATGTGAACCCCATGGGCACTCCAGAAAGAGCAACATTTGCCATTGGC 726
 Qy 629 ATCTCCCTGGCAATATGCTGCTGACCTCTGCTGTCACCATCCCTTTGTATGCTGGAAG 688
 Db 727 ATCTCCCTGGCAATATGCTGCTGACCTCTGCTGTCACCATCCCTTTGTATGCTGGAAG 746
 Qy 689 CAGACATCTTCAATTCCTGCTGCAACATCAACACGCTGATGATGTTTGTGCTGACAG 748

Db		787	CAGACGATCTTCATTCCCTGCGCCCTGAACTACAGACTGTCTATGATGTTTTCCTGAGAG	846
Qy		749	CTCTTGGTGGAGACATGTTCAATTACTTCTCTCTGCGCAATTGGGGTCTTTCTGTTG	808
Db		847	CTCTTGGGGGAGACATGTTCAATTACTTCTCTCTCTCTGCGCAATTGGGGTCTTTCTGTTG	906
Qy		809	CCAGGCTTCCCTCACAGGCTCTGCGCCATGTCGATGATCAAGATGTCGCGATCTTGGCC	868
Db		907	CCAGGCTTCCCTCACAGGCTCTGCGCCATGTCGATGATCAAGATGTCGCGATCTTGGCC	966
Qy		869	ATGATGTAAGAACTCAGAGAAAGAAAGAAAGAGAGGCGCATCAACTATGTCACTGTCCG	928
Db		967	ATGATGTAAGAACTCAGAGAAAGAAAGAAAGAGAGGCGCATCAACTATGTCACTGTCCG	1026
Qy		929	GGCATGTACCTGATCTGCTTCACTCTTAGTAACTTCTGCTTGTGTGTGATTAATTTCTG	988
Db		1027	GGCATGTACCTGATCTGCTTCACTCTTAGTAACTTCTGCTTGTGTGTGATTAATTTCTG	1086
Qy		989	ATTAAAGAGCCGAGGCGCAGAGGCAAGTCTATAGTCCCTGTATCATTTAGACCCCTGTGCTCT	1048
Db		1087	ATTAAAGAGCCGAGGCGCAGAGGCAAGTCTATAGTCCCTGTATCATTTAGACCCCTGTGCTCT	1146
Qy		1049	ACCCCTTAACAGCTGATGAGCCCTCTTGTCTATTACTTGTGTTTCAATGATTTGAGGGAT	1108
Db		1147	ACCCCTTAACAGCTGATGAGCCCTCTTGTCTATTACTTGTGTTTCAATGATTTGAGGGAT	1206
Qy		1109	CATGCAAGAAACGCTCTCTTTGCGGAAGTGTCCGCACTGTAAAGCAGATSCAAGTATCC	1168
Db		1207	CATGCAAGAAACGCTCTCTTTGCGGAAGTGTCCGCACTGTAAAGCAGATSCAAGTATCC	1266
Qy		1169	CTCACCTTAAGAAACATCTCCAGGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT	1228
Db		1267	CTCACCTTAAGAAACATCTCCAGGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT	1326
Qy		1229	AAGACCTCTCTATGAGTTTCCAGGTCCTCGATGGGAATGGCAAGTAGAGTGGAAAC	1288
Db		1327	AAGACCTCTCTATGAGTTTCCAGGTCCTCGATGGGAATGGCAAGTAGAGTGGAAAC	1386
Qy		1289	CTGTTTAATGTTATGAGGACGTGTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAGAA	1348
Db		1387	CTGTTTAATGTTATGAGGACGTGTCTGTTATTTCCGATCCAGATCTTATTTAAAGCAGAA	1446
Qy		1349	C 1349	
Db		1447	C 1447	
RESULT 7				
ADN39780				
ID	ADN39780	standard; cDNA; 1451 BP.		
ADN39780;				
DT	17-JUN-2004	(first entry)		
DE	Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C152.			
XX				
XX				
XX				
KW	Human; differential expression; cancer; angiogenic disorder;			
KW	fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;			
KW	inflammatory disease; autoimmune disease;			
KW	retinal neovascularisation syndrome; scarring; uterine fibroid;			
KW	detection; diagnosis; prognosis; drug screening; drug targeting;			
KW	wound healing; contraception; cytostatic; cardiant; immunomodulatory;			
XX	vulnerary; gene therapy; vaccine; gene; ss.			
OS	Homo sapiens.			
XX				
PN	WO2003042661-A2.			
XX				
PD	22-MAY-2003.			
XX				
PF	13-NOV-2002; 2002WO-US036810.			

PR	13-NOV-2001;	2001US-0356666P.
PR	21-NOV-2001;	2001US-0332466P.
PR	29-NOV-2001;	2001US-0334393P.
PR	03-DEC-2001;	2001US-0335394P.
PR	14-DEC-2001;	2001US-0340376P.
PR	08-JAN-2002;	2002US-0347211P.
PR	10-JAN-2002;	2002US-0347349P.
PR	08-FEB-2002;	2002US-0355250P.
PR	13-FEB-2002;	2002US-0356714P.
PR	20-FEB-2002;	2002US-0359077P.
PR	29-MAR-2002;	2002US-0368809P.
PR	04-APR-2002;	2002US-0370110P.
PR	12-APR-2002;	2002US-0372246P.
PR	05-JUN-2002;	2002US-0386614P.
PR	16-JUL-2002;	2002US-0396839P.
PR	22-JUL-2002;	2002US-0397757P.
PR	09-SEP-2002;	2002US-0409450P.
XX	(EOSB-) EOS BIOTECHNOLOGY INC.	
PA	Afar D., Aziz N., Ginsburg WM., Gish KC., Glynn R., Heyezi PA;	
PI	Mack DH., Murray R., Watson SR., Wilson KE., Zlotnik A;	
Pt	WPI, 2003-468649/44.	
DR	P-PDSB; ADN39997.	
XX	Determining the presence or absence of a pathological cell in a patient,	
PT	useful for diagnosing, prognosing or treating cancer, comprises detecting	
PT	a nucleic acid in a biological sample.	
XX	Claim 8; SEQ ID NO C152; 1385PP; English.	
XX	The invention relates to nucleic acids and proteins (ADN38683-ADNA0064)	
CC	whose expression is upregulated or downregulated in specific cancers or	
CC	other diseases such as angiogenic or fibrotic disorders, and to methods	
CC	of determining the presence or absence of a pathological cell in a	
CC	patient by detecting a nucleic acid at least 80% identical to those of	
CC	the invention or by detecting a polypeptide of the invention. The	
CC	invention also relates to expression vectors and host cells comprising a	
CC	nucleic acid of the invention; antibodies which specifically bind a	
CC	polypeptide of the invention; use of such antibodies for drug targeting;	
CC	and methods of screening for modulators of activity or expression of the	
CC	polypeptides and nucleic acids. The nucleic acids, polypeptides,	
CC	antibodies and methods are useful for diagnosing, prognosing and treating	
CC	cancer and other conditions such as psoriasis, leukaemia, heart disease,	
CC	atherosclerosis, inflammatory diseases, autoimmune diseases, retinal	
CC	neovascularisation syndromes, scarring and uterine fibroids. They may	
CC	also be useful in wound healing and in contraception. The present	
CC	sequence represents a nucleic acid sequence of the invention.	
XX	Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;	
SQ		
Query Match	90.0%; Score 1273; DB 11; Length 1451;	
Best Local Similarity	97.7%; Pred. No. 0;	
Matches 1291; Conservative	0; Mismatches 30; Indels 0; Gaps 0;	
OY	29 GGCGAATTCGATCCAGAGGATCGGAGCCCCACGCGCGCTGGCTGGGGGCCGCC	88
DB	127 GGCGTGGGGCTTCAAGAGGATCGGAGCCCCACGCGCGGTGGCTGGGGGGCGCC	186
OY	89 ATCTGTGATGAGGCTCTCTCTCTCTCGCAGTGGAACAATCCAAAGAACCAATGATCTCT	148
DB	187 ATCTGTGATGAGGCTCTCTCTCTCTCGCAGTGGAACAATCCAAAGAACCAATGATCTCT	246
OY	149 AAAGAGAAGACCCTTATTGGTAAGTTGATGGCACATCCACGTCGACTGGAAAAAGATT	208
DB	247 AAAAGAGAAGACCCTTATTGGTAAGTTGATGGCACATCCACGTCGACTGGAAAAAGATT	306
OY	209 ACACTTAAAAGCTTTTTCTGCTGAGTAGAGTTTCTGCATGTGCTGCTGGAAAAACTG	268
DB	307 ACACTTAAAAGCTTTTTCTGCTGAGTAGAGTTTCTGCATGTGCTGCTGGAAAAACTG	366

QY	269	ACCACTGCTTCCTTCCAAATGCTGACAAATGGTTGGGGTGGTTGCAAGTAAC	328
Db	367	ACCAAGGCTTCTTCACATGCTGACAAATGGTTGGGGTGGTTGCAAGTAAC	426
QY	329	GGCATGAGCCCTAATGGGCTTTCTTTCCGAACTAAGAAAGACCCCTGCTGATTAAC	388
Db	427	GGCAATGGCCCTGTGGGCTTTCTTTCCGAACTAAGAAAGACCCCTGCTGATTAAC	486
QY	389	ATGGCAATCTGGCCCTTGGCTGACCTCCTCTGTGATCTGGTTCCCTTGAAGTTGCC	448
Db	487	ATGGCAATCTGGCCCTTGGCTGACCTCCTCCTGTGATCTGGTTCCCTTGAAGTTGCC	546
QY	449	TATACATATACATGGGAACAATGGAATTAATGGGGAAGCTCTTTGTAATGTCTTAATGGC	508
Db	547	TATACATATACATGGGAACAATGGAATTAATGGGGAAGCTCTTTGTAATGTCTTAATGGC	606
QY	509	TTTTTCTATCGCAATGTAAGTCTTCCATTCCTTCTTCAATGACCTGCTCAGTGTGACAGAG	568
Db	607	TTTTTCTATGCGCAATGTAAGTCTTCCATTCCTTCTTCAATGACCTGCTCAGTGTGACAGAG	666
QY	569	TATTGGGTCACTGTGAACCCCAATGGGGCACTTCAGAGAAAGGCAAACTTGCCATTGGC	628
Db	667	TATTGGGTCACTGTGAACCCCAATGGGGCACTTCAGAGAAAGGCAAACTTGCCATTGGC	726
QY	629	ATCTTCCTGGCAATATGGCTGTGACTCTGTGTGTGACCATTCCTTTGTATGTGCTGAAG	688
Db	727	ATCTTCCTGGCAATATGGCTGTGATTGCTGTGTGACCATTCCTTTGTATGTGCTGAAG	786
QY	689	CAGACCATCTTCAATCTCGCCCTGAAACATACAGACTGTGATGATGTTTGGCTGAGAG	748
Db	787	CAGACCATCTTCAATCTCGCCCTGAAACATACAGACTGTGATGATGTTTGGCTGAGAG	846
QY	749	CTCTTGTGTGGAGACATGTTCAATTACTTCCCTCTCTGAGCCATTGGGGTCTTTCTGTTC	808
Db	847	CTCTTGTGTGGAGACATGTTCAATTACTTCCCTCTCTGAGCCATTGGGGTCTTTCTGTTC	906
QY	809	CCAGCTTCTCTCAACAGCCTCTGCTATGTGCTGATATCAGATAGCTGGATCTTCTGCC	868
Db	907	CCAGCTTCTCTCAACAGCCTCTGCTATGTGCTGATATCAGATAGCTGGATCTTCTGCC	966
QY	869	ATTGATGTAACCTCAGAGAAGAAAGAAAGGGGCATCAAACTGATTGTCACTGTCCCTG	928
Db	967	ATTGATGTAACCTCAGAGAAGAAAGAAAGGGGCATCAAACTGATTGTCACTGTCCCTG	1026
QY	929	GGCATATGACTGATCTGCTTCACTCCTATGTAACCTTCTGCTGTGTGATTAATTTCTG	988
Db	1027	GGCATATGACTGATCTGCTTCACTCCTATGTAACCTTCTGCTGTGTGATTAATTTCTG	1086
QY	989	ATTAAAGACCAGGGCCAGAGCCATGTCTATATGCTCTGATCATTTGAGCCCTCTGCTCTCT	1048
Db	1087	ATTAAAGACCAGGGCCAGAGCCATGTCTATATGCTCTGATCATTTGAGCCCTCTGCTCTCT	1146
QY	1049	ACCCTTAACAGTGCATGACCCCTTTTGTCTATTACTTTGTTTCAATGATTTCAAGGAT	1108
Db	1147	ACCCTTAACAGTGCATGACCCCTTTTGTCTATTACTTTGTTTCAATGATTTCAAGGAT	1206
QY	1109	CATGCAAAAGAAAGCTCTCTCTTGGCCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTACCC	1168
Db	1207	CATGCAAAAGAAAGCTCTCTCTTGGCCGAAGTGTCCGCACTGTAAAGCAGATGCAAGTACCC	1266
QY	1169	CTCACTCAAAAGAAACATCTCCAGAAATTCAGCTCTTACTCTTCAAGTTCAACACTGTT	1228
Db	1267	CTCACTCAAAAGAAACATCTCCAGAAATTCAGCTCTTACTCTTCAAGTTCAACACTGTT	1326
QY	1229	AAGACTCTCTATTTAGTTTTCAGGCTCTCAGATGGGAATTGCACATGATGTGTGAAC	1288
Db	1327	AAGACTCTCTCTATTTAGTTTTCAGGCTCTCAGATGGGAATTGCACATGATGTGTGAAC	1386
QY	1289	CTGTTTAATGTTAATGAGACGCTGTGTTATTTCCGAAATCCAGATCTTAATTAAAGCAAA	1348
Db	1387	CTGTTTAATGTTAATGAGACGCTGTGTTATTTCCGAAATCCAGATCTTAATTAAAGCAAA	1446

OY		1349 C 1349
Pt		1447 C 1447
Db		
<hr/>		
RESULT 8		
ID ADR46617		
ADR46617 standard; DNA; 1451 BP.		
XX AC		ADR46617;
XX DT		18-NOV-2004 (first entry)
DE XX		Cancer-associated protein coding sequence, SEQ ID 30.
KW XX		Cytostatic; Gene Therapy; cancer; human; gene; ds.
OS XX		Homo sapiens.
FH Key		Location/Qualifiers
FT CDS		/tag= 148..1341
PT FT		/product= "Cancer-associated protein, SEQ ID 88"
PN MO2004073657-A2.		
PD 02-SEP-2004.		
PF 19-FEB-2004; 2004WO-US005455.		
PR 19-FEB-2003; 2003US-0448784P.		
PA (PROT-) PROTEIN DESIGN LABS INC.		
PI Aziz N., Gish KC, Wilson KE, Zlotnick A,		
PI WPJ; 2004-652787/63.		
PK P-PSTDB; ADR46675.		
XX DR		Detecting a pathological cell in a patient for diagnosing or treating
XX PT		cancer by detecting in a biological sample from the patient genes whose
XX PR		expression are up-regulated or down-regulated in specific cancers.
PS Claim 1; SEQ ID NO 30; 375bp; English.		
CC The present invention relates to a method for detecting cancer in a		
CC patient. The method comprises detecting in a biological sample from the		
CC patient a nucleotide or protein sequence comprising a sequence that is at		
CC least 80% identical to a nucleotide sequence (ADK46588-ADK4645) or		
CC protein sequence (ADK46646-ADK46703). The method is useful for detecting		
CC cancer for preparing a composition for diagnosis or treating cancer.		
SQ Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other:		
Query Match	90.0%; Score 1273; DB 13; Length 1451;	
Best Local Similarity	97.7%; Pred. No. 0;	
Matches 1291; Conservative 0; Mismatches 30; Indels 0; Gaps 0;		
OY	29 GGCGAATTGGATACGAGAGAATGCCGAAGCCCCGCAGGTCTGTGGGGGGCGCC	88
Db	127 GGCCTTCGGGGCTTCAGAGAGATCCGAGCCCAGCCGGGCTGTGCTGGGGGGCGCC	186
OY	89 ATCTGTAGCAAGCCTCTCTCTCTTGAGTAGGCACCATCCAAAGAACATAATAGTCTCT	148
Db	187 ATTCTGTAGCAAGCCTCTCTCTCTCTGCAGTGGCACCATCCAAAGAACATAATAGTCTCT	246
OY	149 AAAGAAAAGACCCTTAATTGGTTGATGGATGACAATCCACTCTGAAAAAGAGTT	208
Db	247 AAAAGAAAAGACCCTTAATTGGTTGATGGATGACAATCCACTCTGAAAAAGAGTT	306
OY	209 ACAATTGAAAACGCTTTTTCTGTGGAGAGAGTTTTCTGCATCTGTCTCGCTGAAAACTG	268
Db	307 ACAATTGAAAACGCTTTTTCTGTGGAGAGAGTTTTCTGCATCTGTCTCGCTGAAAACTG	366

OY	269	ACACGTGCTTCCTTCAAAATGTCACAAATGTTGTGGGATGGTTGGCAAGTAC	328
Db	367	ACCAAGGCTTCTTCCAAATGTCTACACAAATGTTGTGGATGGTTGGCAAGTAC	426
OY	329	GGCATAGGCCCAATGGGTCTTCTTTCGGAATGAAGAACACCTGCTGTATTTAC	388
Db	427	GGCATAGGCCCTGTGGGTCTTCTTTCGGAATGAAGAACACCTGCTGTATTTAC	486
OY	389	ATGGCAATCTGGCCTTGGCTGACCTCTCTCTGTCACTGTGTCCCTTGAAGATTGCC	448
Db	487	ATGGCAATCTGGCCTTGGCTGACCTCTCTCTGTCACTGTGTCCCTTGAAGATTGCC	546
OY	449	TATCACTATACATGACACAACTGATTTATGGGGAAGCTCTTGTGAATGTCTTATGGC	508
Db	547	TATCACTATACATGACACAACTGATTTATGGGGAAGCTCTTGTGAATGTCTTATGGC	606
OY	509	TTTTTCTATCGCAACATGTACTGTTCATCTCTTCAATGACCTGCTCAATGTGACAGG	568
Db	607	TTTTTCTATCGCAACATGTACTGTTCATCTCTTCAATGACCTGCTCAATGTGACAGG	666
OY	569	TATTGGGATCATGCGTAACCCCAATGGGGACATCAGAGAAAGGCAAACTTGGCATTGGC	628
Db	667	TATTGGGATCATGCGTAACCCCAATGGGGACATCAGAGAAAGGCAAACTTGGCATTGGC	726
OY	629	ATCTCCCTGGCAATATGAGCTGTGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	688
Db	727	ATCTCCCTGGCAATATGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	786
OY	689	CAGACCATCTTCATCTCCCTGACCTGTAACATCAGACCTGTCAATGATGTTTGGCTGAGAG	748
Db	787	CAGACCATCTTCATCTCCCTGACCTGTAACATCAGACCTGTCAATGATGTTTGGCTGAGAG	846
OY	749	CTCTGTGTGGAGACATGTTCAATTACTTCTCTCTCTGTGGCATTTGGGGTCTTCTGTTC	808
Db	847	CTCTGTGTGGAGACATGTTCAATTACTTCTCTCTCTGTGGCATTTGGGGTCTTCTGTTC	906
OY	809	CCAGCTTCTTCACAGCTCTGTGCTTATGTGCTGATGATCAGAAATGCTGCCATCTTCTGCC	868
Db	907	CCAGCTTCTTCACAGCTCTGTGCTTATGTGCTGATGATCAGAAATGCTGCCATCTTCTGCC	966
OY	869	ATGATGAAAACTCAGAGAAAGAAAGAAAGAGGGGCATCAAACTGATGTCACTGTCTCG	928
Db	967	ATGATGAAAACTCAGAGAAAGAAAGAAAGAGGGGCATCAAACTGATGTCACTGTCTCG	1026
OY	929	GGCATGTACTGTATCTGTCTCACTCTCTGTAGTAACTTCTGTGTGTGTGTGTGTGTGTGTGT	988
Db	1027	GGCATGTACTGTATCTGTCTCACTCTCTGTAGTAACTTCTGTGTGTGTGTGTGTGTGTGTGT	1086
OY	989	ATTAGAGCCAGGGGCGAGAGCAATGTCTAATGCCGTGTACTTGTAGCCCTGTGCTCTCT	1048
Db	1087	ATTAGAGCCAGGGGCGAGAGCAATGTCTAATGCCGTGTACTTGTGTAGCCCTGTGCTCTCT	1146
OY	1049	ACCCTTAAAGCTGTGATGACCCCTTGTGTCTAATTACTTGTGTGTGTGTGTGTGTGTGTGTGT	1108
Db	1147	ACCCTTAAAGCTGTGATGACCCCTTGTGTCTAATTACTTGTGTGTGTGTGTGTGTGTGTGTGT	1206
OY	1109	CATGAAAGAAAGCTCTCTCTTGTGCCAAGTGTGCCGACTGTATAGCAAGATGTCACTGTACC	1168
Db	1207	CATGAAAGAAAGCTCTCTCTTGTGCCAAGTGTGCCGACTGTATAGCAAGATGTCACTGTACC	1266
OY	1169	CTCACTCAAAAGAAACATCTCCAGAAATTCAGACTCTTACTCTTCAAGTTCAACCACTGT	1228
Db	1267	CTCACTCAAAAGAAACATCTCCAGAAATTCAGACTCTTACTCTTCAAGTTCAACCACTGT	1326
OY	1229	AAGACCTCCATATGATTTTCCAGGTCTCCAGATGGGAATTGCACAGTAGAATGTGTAAC	1288
Db	1327	AAGACCTCCATATGATTTTCCAGGTCTCCAGATGGGAATTGCACAGTAGAATGTGTAAC	1386
OY	1289	CTGTTTATNGTATAGAGACGATCTGTATTTCCGATGCCAGATCTTATTAAGACAA	1348
Db	1387	CTGTTTATNGTATAGAGACGATCTGTATTTCCGATGCCAGATCTTATTAAGACAA	1446

QY	1349	C 1349
Db	1447	C 1447
RESULT 9		
ADST74019		
ID	ADST74019	standard; cDNA; 1451 BP.
XX		
AC	ADST74019;	
XX		
DT	16-DEC-2004	(first entry)
XX		
DE	Human G-protein coupled proteinase activated receptor 2 polynucleotide.	
XX		
KW	Human; proteinase activated receptor 2; PAR2; G-protein coupled receptor;	
KW	receptor; cardiac; neuroprotective; nephrotoxic; respiratory-gen. ;	
KW	gastrointestinal-gen. ; gene therapy; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
XX		
FT	CDS	148..1341
FT		/*tag= a
FT		/product= "Human PAR2"
XX		
FN	WO2004080373-A2.	
XX		
PD	23-SEP-2004.	
XX		
PF	26-FEB-2004; 2004WO-EP001896.	
XX		
PR	11-MAR-2003; 2003EP-00004980.	
XX		
PA	(FARB) BAYER HEALTHCARE AG.	
XX		
PI	Golz S, Brueggemeier U, Summer H;	
XX		
DR	WPI; 2004-677358/66.	
XX		
DR	P-PSDB; ADST74020.	
XX		
PT	Screening for therapeutic agents for treating e.g., cardiovascular	
PT	diseases by contacting a test compound with a proteinase activated	
PT	receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of	
PT	the test compound.	
XX		
PS	Disclosure; SEQ ID NO 1; 121pp; English.	
XX		
CC	The present sequence is that of a polynucleotide encoding G-protein	
CC	coupled proteinase activated receptor 2 (PAR2). PAR2 is an	
CC	antiinflammatory receptor in the colon and may also play a role in the	
CC	airway, regulating sodium ion absorption and anion secretion. The	
CC	invention relates to novel disease associations of PAR2 polypeptides and	
CC	polynucleotides. It also relates to novel methods of screening for	
CC	therapeutic agents for the treatment of cardiovascular disorders,	
CC	gastrointestinal and liver diseases, neurological disorders, urological	
CC	disorders, hematological diseases and respiratory diseases in a mammal.	
CC	Suitable therapeutic agents include a small molecule, an RNA molecule, an	
CC	antisense oligonucleotide, a polypeptide, an antibody or a ribozyme. The	
CC	invention also provides pharmaceutical compositions for the treatment of	
CC	diseases and disorders associated with PAR2 comprising a PAR2	
CC	polypeptide, PAR2 polynucleotide or a regulator or modulator of PAR2	
CC	activity. Methods of diagnosing these diseases and disorders involve	
CC	determining the amount of PAR2 polynucleotide in a sample.	
XX		
SQ	Sequence 1451 BP; 310 A; 389 C; 346 G; 406 T; 0 U; 0 Other;	
Query Match	90.0%; Score 1273; DB 13; Length 1451;	
Best Local Similarity	97.7%; Pred. No. 0;	
Matches 1291;	Conservative 0; Mismatches 30; Indels 0; Gaps 0;	
29	GCGCAATTCGATCCAGAGATCCGAGACCCACGCGCGCTGCTGCTGCGGCGCGCC 88	

Db 127 GGGCTGGGGCTTCAAGAGGATGCGAGGCCGAGCGGGCTGCTGCGGGCCGCC 186
 Qy ATCTCTGACACCTCTCTCTCTGAGTGGCACTCCAGGAACCAATAGATCTCT 148
 Db 187 ATCTCTGACACCTCTCTCTCTGAGTGGCACTCCAGGAACCAATAGATCTCT 246
 Qy 149 AAGAGGAAGAGCTTATGTTAGTGAAGTGAAGCATCCACGCTCATGGAAGAGATT 208
 Db 247 AAGAGGAAGAGCTTATGTTAGTGAAGTGAAGCATCCACGCTCATGGAAGAGATT 306
 Qy 209 ACAGTTGAAACAGCTTTTCTGTGATGAGATTTTCTGCACTCTGCTGCTGAAACCTG 268
 Db 307 ACAGTTGAAACAGCTTTTCTGTGATGAGATTTTCTGCACTCTGCTGCTGAAACCTG 366
 Qy 269 ACCAGCTCTCTCTCTCTGCAATTTGCTCAACAATTTGTTGGGGTGGTTCAGATAC 328
 Db 367 ACCAGCTCTCTCTCTCTGCAATTTGCTCAACAATTTGTTGGGGTGGTTCAGATAC 426
 Qy 329 GGCATGGCCCTATGGGTCTTCTTTTCCGAACCTAAGAGAGACCTGCTGATTTAC 388
 Db 427 GGCATGGCCCTATGGGTCTTCTTTTCCGAACCTAAGAGAGACCTGCTGATTTAC 486
 Qy 389 ATGGCCATCTGGCCTTGGCTGACCTCTCTGTCATCTGTTCCCTTGAAGATTGCC 448
 Db 487 ATGGCCATCTGGCCTTGGCTGACCTCTCTGTCATCTGTTCCCTTGAAGATTGCC 546
 Qy 449 TATCACAATATGAGCAACATGATTTATGAGGAAGCTCTTTGTAATGCTTATGGC 508
 Db 547 TATCACAATATGAGCAACATGATTTATGAGGAAGCTCTTTGTAATGCTTATGGC 606
 Qy 509 TTTTTCATGCAACATGATCTGTTTCAATCTCTTCAATGACCTGCTGATGTCAGAGG 568
 Db 607 TTTTTCATGCAACATGATCTGTTTCAATCTCTTCAATGACCTGCTGATGTCAGAGG 666
 Qy 569 TATTGGGATCATGTGAACCCCATGGGGCACTCCAGAGAGAGCAACATTGCCATTGGC 628
 Db 667 TATTGGGATCATGTGAACCCCATGGGGCACTCCAGAGAGAGCAACATTGCCATTGGC 726
 Qy 629 ATCTCCCTGGCAATATGAGTGTGCTGATCTGTGTCACATCCCTTTGTAATGCTGAAG 688
 Db 727 ATCTCCCTGGCAATATGAGTGTGCTGATCTGTGTCACATCCCTTTGTAATGCTGAAG 786
 Qy 689 CAGACCATCTTCAATCTGCTGCTGAACATGACGACCTGATGATGTTTGGCTGAGACAG 748
 Db 787 CAGACCATCTTCAATCTGCTGCTGAACATGACGACCTGATGATGTTTGGCTGAGACAG 846
 Qy 749 CTCCTGGTGGAGACATGTTCAATTAATCTCTCTCTGACCATGAGGATCTTCTGTTTC 808
 Db 847 CTCCTGGTGGAGACATGTTCAATTAATCTCTCTCTGACCATGAGGATCTTCTGTTTC 906
 Qy 809 CCGAGCTTCTTCAACAGCTCTGCTGATGCTGATGATGATGATGCTGCAATCTTCTGCC 868
 Db 907 CCGAGCTTCTTCAACAGCTCTGCTGATGCTGATGATGATGATGCTGCAATCTTCTGCC 966
 Qy 869 ATGAGTGAACACTCAG 928
 Db 967 ATGAGTGAACACTCAG 1026
 Qy 929 GGCATGATCTGATCTGCTTCACTCTGATGATCTTCTGCTGTGATGATGATGATGATGAT 988
 Db 1027 GGCATGATCTGATCTGCTTCACTCTGATGATCTTCTGCTGTGATGATGATGATGATGAT 1086
 Qy 989 ATTAAGAGCGAGGCGAG 1048
 Db 1087 ATTAAGAGCGAGGCGAG 1146
 Qy 1049 ACCCTTAACAGCTGATGACCCCTTGTGATGATCTTCTGATGATGATGATGATGATGAT 1108
 Db 1147 ACCCTTAACAGCTGATGACCCCTTGTGATGATCTTCTGATGATGATGATGATGATGAT 1206
 Qy 1109 CATGCAAGAGAGCTCTCTTGTGCGAGAGTGTGCGACCTGTAAGAGAGATGACAGTACC 1168
 Db 1207 CATGCAAGAGAGCTCTCTTGTGCGAGAGTGTGCGACCTGTAAGAGAGATGACAGTACC 1266

Qy 1169 CTCACCTCAAG 1228
 Db 1267 CTCACCTCAAG 1326
 Qy 1229 AAGACCTCTATGAGTGTTCAGAGTCTTCAGATGAGAGAGAGAGAGAGAGAGAGAG 1288
 Db 1327 AAGACCTCTATGAGTGTTCAGAGTCTTCAGATGAGAGAGAGAGAGAGAGAGAGAG 1386
 Qy 1289 CTGTTTAATGATGAG 1348
 Db 1387 CTGTTTAATGATGAG 1446
 Qy 1349 C 1349
 Db 1447 C 1447
 RESULT 10
 ABZ35045
 ID ABZ35045 standard; cDNA; 2848 BP.
 AC ABZ35045;
 DT 05-FEB-2003 (first entry)
 XX
 DE Human gene expression profile polynucleotide SEQ ID NO 157.
 XX
 KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
 KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
 KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
 KW gene expression; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200274979-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 20-MAR-2002; 2002MO-US008456.
 XX
 PR 20-MAR-2001; 2001US-0276947P.
 XX
 PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
 XX
 PI Wan J, Wang Y;
 XX
 DR WPI; 2002-740862/80.
 XX
 PT New gene expression profile generated from primary, endothelial,
 PT epithelial, and muscle cell types, useful for identifying disease
 PT pathologies involving alterations of gene expression, e.g. cancer.
 XX
 PS Claim 3; Page 381-382; 850bp; English.
 XX
 CC The invention relates to a gene expression profile comprising one or more
 CC genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
 CC is a coronary artery endothelium, umbilical artery or vein endothelium,
 CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
 CC endothelium, myometrium microvascular endothelium, keratinocyte
 CC epithelium, bronchial epithelium, mammary epithelium, prostate
 CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
 CC small airway epithelium, renal epithelium, umbilical artery smooth
 CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
 CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
 CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
 CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
 CC osteoblasts or prostate stromal cell. The gene expression profile is
 CC for determining the level of RNA expression for a sample, determining the
 CC phenotype of a cell and distinguishing cell types. The gene or a protein
 CC expression profile is useful in identifying disease pathologies involving
 CC alterations of gene expression. The assessment of expression profiles may
 CC provide meaningful information with respect to tumour type and stage.

CC treatment methods, and prognosis. The gene or protein expression profile
CC may also be used for creating microarrays. The microarray is useful for
CC genetic and physical mapping of genomes, DNA sequencing, genetic or
CC medical diagnosis, genotyping of organisms, confirming cell or tissue
CC identifications and in identifying promising antibiotics, antiviral or
CC antifungal agents

SQ Sequence 2848 BP; 670 A; 562 C; 552 G; 771 T; 0 U; 293 Other;

Query Match 89.4%; Score 1263.6; DB 6; Length 2848;
Best Local Similarity 97.4%; Pred. No. 0;
Matches 1295; Conservatve 0; Mismatches 34; Indels 1; Gaps 1;

QY 29 GGGGAATTCGGATTCAGAGAGATCGAGAGCCGAGCGCGGCTGCTGGGGCGCC 88
DB 126 GGGGTGGGGCTTCCAGAGAGATCGAGAGCCGAGCGCGGCTGCTGGGGCGCC 185
QY 89 ATCTCTCTAGACGCTCTCTCTCTGCAATGAGCAATCCAGAACCAATTAATCTCT 148
DB 186 ATCTCTCTAGACGCTCTCTCTCTGCAATGAGCAATCCAGAACCAATTAATCTCT 245
QY 149 AAGAGAGAGAGCTTATGTTAGTTGATGAGCAATCCAGAACCAATTAATCTCT 207
DB 246 AAGAGAGAGAGCTTATGTTAGTTGATGAGCAATCCAGAACCAATTAATCTCT 305
QY 208 TACAGTTGAAACAGCTCTTCTCTGAGTGAATTTCTGCAATCTGCTGCGTGGAAACT 267
DB 306 TACAGTTGAAACAGCTCTTCTCTGAGTGAATTTCTGCAATCTGCTGCGTGGAAACT 365
QY 268 GACCACTGCTCTCTCTCTGCAATTTGTTGTTGGGTTGGGTTGGCAAGTAA 327
DB 366 GACCACTGCTCTCTCTCTGCAATTTGTTGTTGGGTTGGGTTGGCAAGTAA 425
QY 328 CGGATGAGCCCTATGAGTCTTCTTCTTCCGAACTAAGAGAGACGCTGCTGATTTA 387
DB 426 CGGATGAGCCCTATGAGTCTTCTTCTTCCGAACTAAGAGAGACGCTGCTGATTTA 485
QY 388 CATGAGCAATCTGAGCTTGGCTGAGCTCTCTCTGATCTGCTGCTTCCCTTGAAGTTGG 447
DB 486 CATGAGCAATCTGAGCTTGGCTGAGCTCTCTCTGATCTGCTGCTTCCCTTGAAGTTGG 545
QY 448 CTATCATCATCATGAGCAACATGATTTATGAGGAGAGCTCTTGTATGTCTTATTTGG 507
DB 546 CTATCATCATCATGAGCAACATGATTTATGAGGAGAGCTCTTGTATGTCTTATTTGG 605
QY 508 CTTTCTCTATGCAATGATGATGCTTCATCTCTTCATGACCTGCTCAGTGTGAGAG 567
DB 606 CTTTCTCTATGCAATGATGATGCTTCATCTCTTCATGACCTGCTCAGTGTGAGAG 665
QY 568 GATTTGGGTCATGCTGAACCCCATGAGGAGCTCAGAGAGAGAGCAAACTTGCATTGG 627
DB 666 GATTTGGGTCATGCTGAACCCCATGAGGAGCTCAGAGAGAGAGCAAACTTGCATTGG 725
QY 628 CATCTCTCTGAGCAATGAGTGTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 687
DB 726 CATCTCTCTGAGCAATGAGTGTGCTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 785
QY 688 GAGACCATCTTCAATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 747
DB 786 GAGACCATCTTCAATCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 845
QY 748 GCTCTTGTGAGAGACATGCTTCAATCTCTCTCTGAGCAATGAGGCTCTTCTGCTT 807
DB 846 GCTCTTGTGAGAGACATGCTTCAATCTCTCTCTGAGCAATGAGGCTCTTCTGCTT 905
QY 808 CCGAGCTTCTCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867
DB 906 CCGAGCTTCTCTCAAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 965
QY 868 CATGATGAGAAATCTCAG 927
DB 966 CATGATGAGAAATCTCAG 1025

QY 928 GGGCATGTAAGTATGCTGCTTCACTCTGATGTAACCTTCTGCTTGGTGCATTTATTTCT 987
DB 1026 GGGCATGTAAGTATGCTGCTTCACTCTGATGTAACCTTCTGCTTGGTGCATTTATTTCT 1085
QY 988 GATTAAAGCCAGGGGAGAGAGATGTCATGCTGCTGATGTAAGCTTGCAGCTGCTGCTG 1047
DB 1086 GATTAAAGCCAGGGGAGAGAGATGTCATGCTGCTGATGTAAGCTTGCAGCTGCTGCTG 1145
QY 1048 TACCTTTAAACAGCTGATGAGACCCCTTGTCTATTAATCTTGTGTTTCAATGATTTTCA 1107
DB 1146 TACCTTTAAACAGCTGATGAGACCCCTTGTCTATTAATCTTGTGTTTCAATGATTTTCA 1205
QY 1108 TCATGTAAGAAAGCTCTCTCTTCCGAGAGTGTCCGACATGTAAGCAATGCAAGTAC 1167
DB 1206 TCATGTAAGAAAGCTCTCTCTTCCGAGAGTGTCCGACATGTAAGCAATGCAAGTAC 1265
QY 1168 CCTCACTCAAGAAACAATCCAGAGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT 1227
DB 1266 CCTCACTCAAGAAACAATCCAGAGAAATCCAGCTCTTACTCTTCAAGTTCAACCACTGT 1325
QY 1228 TAAGACCTCTTATGATGTTTCCAGGTCCTCAGATGGAATTTGCAAGTGAATGTGAA 1287
DB 1326 TAAGACCTCTTATGATGTTTCCAGGTCCTCAGATGGAATTTGCAAGTGAATGTGAA 1385
QY 1288 CCTGTTTAATGTTATGAGAGAGCTGTCTGTTATTTCCGATCCAGATCTTATTTAAAGCA 1347
DB 1386 CCTGTTTAATGTTATGAGAGAGCTGTCTGTTATTTCCGATCCAGAGAGCTCACCACATA 1445
QY 1348 ACTGTTTAT 1357
DB 1446 CCAATGTGAT 1455

RESULT 11
AAD4437
ID AAD4437 standard; DNA; 8624 BP.
XX
AC AAD4437;
XX
DT 13-DEC-2002 (first entry)
XX
DB Human coagulation factor II (thrombin) receptor like 1 (F2RL1) gene.
XX
KW Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;
KW polymorphism; chronic pulmonary disease; inflammatory disorder;
KW gene therapy; gene; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT variation /tag= a
FT /note= "Polymorphic site; PS1"
FT replace(553, C)
FT /tag= b
FT /note= "Polymorphic site; PS2"
FT replace(768, T)
FT /tag= c
FT /note= "Polymorphic site; PS3"
FT replace(850, T)
FT /tag= d
FT /note= "Polymorphic site; PS4"
FT replace(852, G)
FT /tag= e
FT /note= "Polymorphic site; PS5"
FT 1001..7382
FT /tag= f
FT /product= "Human F2RL1 protein"
FT 1001..1082
FT /tag= g
FT /number= 1
FT 1083..6270
FT /tag= h
FT Intron

FT exon 6271..7382
 FT /*tag= 1
 FT /number= 2
 FT variation replace(6277, G)
 FT /*tag= 1
 FT /note= "Polymorphic site; PS6"
 FT replace(6809, T)
 FT /*tag= k
 FT /note= "Polymorphic site; PS7"
 FT replace(7460, C)
 FT /*tag= 1
 FT /note= "Polymorphic site; PS8"
 XX MO200255534-A2.
 XX 18-JUL-2002.
 XX 13-NOV-2001; 2001WO-US046475.
 XX 10-NOV-2000; 2000US-0247516P.
 XX (GENA-) GENA155ANCB PHARM INC.
 XX Bieganski KM, Sanchez A, Shah N;
 XX WPI; 2002-566728/60.
 XX P-PSDB; AA26678.
 XX
 PT New genetic variants having polymorphisms in the coagulation factor II
 PT (thrombin) receptor like 1 (F2RL1) gene, useful for studying the function
 PT of F2RL1 and treating disorders associated with abnormal expression or
 PT function of F2RL1.
 XX
 PS Claim 18; Fig 1; 65p; English.
 XX
 CC The invention relates to an isolated polynucleotide comprising genes and
 CC haplotypes of the coagulation factor II (thrombin) receptor like 1
 CC (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in
 CC studying the expression and biological function of F2RL1, and in
 CC identifying drugs targeting F2RL1 protein for treating disorders
 CC associated with abnormal expression or function of F2RL1, e.g. asthma,
 CC chronic pulmonary disease, and inflammatory disorders. Polynucleotides
 CC comprising a polymorphic gene variant or fragment may be used for
 CC therapeutic purposes, where a patient could benefit from expression or
 CC increased expression of a particular F2RL1 protein isoform, or an
 CC expression vector encoding the isoform may be administered to the
 CC patient. Haplotype information is useful in improving the efficiency and
 CC output of several steps in drug discovery and development process,
 CC including target validation, identifying lead compounds, and early phase
 CC clinical trials. Information on polymorphisms may be applied in studying
 CC biological functions of F2RL1 as well as in identifying drugs targeting
 CC this protein for the treatment of disorders related to its abnormal
 CC expression or function. The invention is useful in gene therapy. The
 CC present sequence is human F2RL1 gene
 XX
 SO Sequence 8624 BP; 2126 A; 2010 C; 1988 G; 2392 T; 0 U; 108 Other;
 Query Match 84.0%; Score 1188.4; DB 6; Length 8624;
 Best Local Similarity 97.8%; Pred. No. 0;
 Matches 1201; Conservative 3; Mismatches 24; Indels 0; Gaps 0;
 QY 130 AGGAAACCAATGATCTCTTAAGAGAGAGACCTTATTGTTGATGACACATCCCA 189
 DB AGGAAACCAATGATCTCTTAAGAGAGAGACCTTATTGTTGATGACACATCCCA 6328
 QY 190 CGTCACTGAAAAAGAGATTACAGTTGAACAGCTCTTTCTGTGATGAGTTTCTGATC 249
 DB CGTCACTGAAAAAGAGATTACAGTTGAACAGCTCTTTCTGTGATGAGTTTCTGATC 6388
 QY 250 TGTCTCTGCTGAAAACTGACCACTGCTCTTCTTCAATTGCTACCAATTGCTTTC 309
 DB TGTCTCTGCTGAAAACTGACCACTGCTCTTCTTCAATTGCTACCAATTGCTTTC 6448

QY 310 GGTGGGTTTCCAGATGACGGGATGAGCCCTATGGCTTTCTTTCCGAATGAAGAA 369
 DB GGTGGGTTTCCAGATGACGGGATGAGCCCTATGGCTTTCTTTCCGAATGAAGAA 6508
 QY 370 GCAACCTGCTGATTTTACATGAGCCATCTGAGCTTGTGACCTCTCTGATCTG 429
 DB GCAACCTGCTGATTTTACATGAGCCATCTGAGCTTGTGACCTCTCTGATCTG 6568
 QY 430 GTTCCCTTGAATATGACCTTATGACATGACATGACATGACATGACATGACATG 489
 DB GTTCCCTTGAATATGACCTTATGACATGACATGACATGACATGACATGACATG 6628
 QY 490 TTGTAATGTCCTATTTGCTTTTCTTATGACATGACATGACATGACATGACATG 549
 DB TTGTAATGTCCTATTTGCTTTTCTTATGACATGACATGACATGACATGACATG 6688
 QY 550 CTGCTCACTGATGACAGATGATGAGGATGATGAGGATGATGAGGATGATGAGG 609
 DB CTGCTCACTGATGACAGATGATGAGGATGATGAGGATGATGAGGATGATGAGG 6748
 QY 610 GGCACATTTGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 669
 DB GGCACATTTGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 6808
 QY 6749 GGCACATTTGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 6808
 DB GGCACATTTGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 6868
 QY 670 CCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 729
 DB CCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6868
 QY 730 TGAATTTTGGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 789
 DB TGAATTTTGGCTGATGAGGATGATGAGGATGATGAGGATGATGAGGATGATGAG 6928
 QY 790 CATTTGGGCTTTTCTGTTCCACCTTCTCAAGCTCTGCTGATGATGATGATGATG 849
 DB CATTTGGGCTTTTCTGTTCCACCTTCTCAAGCTCTGCTGATGATGATGATGATG 6928
 QY 850 AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 909
 DB AATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7048
 QY 910 ACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 969
 DB ACTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7108
 QY 970 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1029
 DB TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7168
 QY 1030 TGTAGCCCTGCTGCTCTTACCTTAAAGAGGATGATGATGATGATGATGATGATG 1089
 DB TGTAGCCCTGCTGCTCTTACCTTAAAGAGGATGATGATGATGATGATGATGATG 7228
 QY 1090 TTGACATGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1149
 DB TTGACATGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 7288
 QY 1150 AAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1209
 DB AAAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7348
 QY 1210 TTGACATGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 1269
 DB TTGACATGATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATG 7408
 QY 1270 GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1329
 DB GCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7468
 QY 1330 AGATCTTATTTAAAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 1357
 DB AGATCTTATTTAAAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 7496

Query Match	83.6%	Score 1182.8	DB 6	Length 1194
Best Local Similarity	99.4%	Pred No. 0		
Result 12				
AA044438				
AA044438 standard; DNA; 1194 BP.				
AA044438;				
13-DEC-2002 (first entry)				
Human coagulation factor II (thrombin) receptor like 1 (F2RL1) DNA.				
Human; haplotype; coagulation factor II receptor like 1; F2RL1; asthma;				
polymorphism; chronic pulmonary disease; inflammatory disorder;				
gene therapy; gene; ds.				
Homo sapiens.				
Key	Location/Qualifiers			
CDS	1..1194			
	/*tag= a			
	/product= "Human F2RL1 protein"			
	replace(89, G)			
	/*tag= b			
	/note= "Polymorphic site"			
	replace(621, T)			
	/*tag= C			
	/note= "Polymorphic site"			
WO200255534-A2.				
18-JUL-2002.				
13-NOV-2001; 2001WO-US046475.				
10-NOV-2000; 2000US-0247516P.				
(GENA-) GENA1SSANCE PHARM INC.				
Bieglecki KM, Sanchis A, Shah N;				
WPI; 2002-566728/60.				
P-PSDB; AAE26678.				
New genetic variants having polymorphisms in the coagulation factor II (thrombin) receptor like 1 (F2RL1) gene, useful for studying the function of F2RL1 and treating disorders associated with abnormal expression or function of F2RL1.				
Claim 23; Fig 2; 65pp; English.				
The invention relates to an isolated polynucleotide comprising genes and haplotypes of the coagulation factor II (thrombin) receptor like 1 (F2RL1) gene. Polymorphic variants of the F2RL1 gene are useful in studying the expression and biological function of F2RL1, and in identifying drugs targeting F2RL1 protein for treating disorders associated with abnormal expression or function of F2RL1, e.g. asthma, chronic pulmonary disease, and inflammatory disorders. Polynucleotides comprising a polymorphic gene variant or fragment may be used for therapeutic purposes, where a patient could benefit from expression or increased expression of a particular F2RL1 protein isoform, or an expression vector encoding the isoform may be administered to the patient. Haplotype information is useful in improving the efficiency and output of several steps in drug discovery and development process, including target validation, identifying lead compounds, and early phase clinical trials. Information on polymorphisms may be applied in studying biological functions of F2RL1 as well as in identifying drugs targeting this protein for the treatment of disorders related to its abnormal expression or function. The invention is useful in gene therapy. The present sequence is human F2RL1 DNA				
Sequence 1194 BP; 264 A; 321 C; 261 G; 348 T; 0 U; 0 Other;				

Matches 1187; Conservative 0; Mismatches 7; Indels 0; Gaps 0				
QY	50	ATGCGAGAGCCCAAGCGGCGTGGCTGCTGCGGAGGCCCGCATCTGCTAGACGCTCTCTC	109	
Db	1	ATGCGAGAGCCCAAGCGGCGTGGCTGCTGCGGAGGCCCGCATCTGCTAGACGCTCTCTC	60	
QY	110	TCCTCGAGTGGCACATCCACGAAACCAATGATCTCTTAAGGAAGAGCCTAATGGT	169	
Db	61	TCCTCGAGTGGCACATCCACGAAACCAATGATCTCTTAAGGAAGAGCCTAATGGT	120	
QY	170	AAGGTGATGSCACATCCACGCTGCTGAGAAAGAGTTACAGTTGAAACAGTCTTTCT	229	
Db	121	AAGGTGATGSCACATCCACGCTGCTGAGAAAGAGTTACAGTTGAAACAGTCTTTCT	180	
QY	230	GTGATGATGTTTCTGACATCTGCTCGTGGAAAACCTGACCACTGTCTTCTTCAAT	289	
Db	181	GTGATGATGTTTCTGACATCTGCTCGTGGAAAACCTGACCACTGTCTTCTTCAAT	240	
QY	290	GTCACACAAATTGTTTGCGGTGGGTTTGCAAGTAAACGCAATGGCCCTAATGGTCTTT	349	
Db	241	GTCACACAAATTGTTTGCGGTGGGTTTGCAAGTAAACGCAATGGCCCTGAGGTCTTT	300	
QY	350	CTTTCCGAACCTAAGAAAGAGCAACCCGCTGCTGATTTAATATGGGCAATCTGAGCCTTGACT	409	
Db	301	CTTTCCGAACCTAAGAAAGAGCAACCCGCTGCTGATTTAATATGGGCAATCTGAGCCTTGACT	360	
QY	410	GACCTCCTCTCTGATCTGTTGCCCTTGAAAGATTGCTATCAATATAGGCAACAC	469	
Db	361	GACCTCCTCTCTGATCTGTTGCCCTTGAAAGATTGCTATCAATATAGGCAACAC	420	
QY	470	TGATTTATAGGGGAAGCTCTTTGTAATGTCTAATGGCTTTTCTAATGCAATGTAC	529	
Db	421	TGATTTATAGGGGAAGCTCTTTGTAATGTCTAATGGCTTTTCTAATGCAACATGTAC	480	
QY	530	TGTTCCATTCCTCTCATGACCTGCTCAGTGTGAGAGGTATATGGGTATGCTGAACCCC	589	
Db	481	TGTTCCATTCCTCTCATGACCTGCTCAGTGTGAGAGGTATATGGGTATGCTGAACCCC	540	
QY	590	ATGGGGCACTCCAGAAAGAAAGCAAAATTTGCCATTTGGCATCTCCCTGGCAATATGGCTG	649	
Db	541	ATGGGGCACTCCAGAAAGAAAGCAAAATTTGCCATTTGGCATCTCCCTGGCAATATGGCTG	600	
QY	650	CTGACTCTGCTGTACCAATCCCTTTGTATGTCTGAAAGCAGACATTTTCAATCTGTCC	709	
Db	601	CTGATTCCTGCTGTACCAATCCCTTTGTATGTCTGAAAGCAGACATTTTCAATCTGTCC	660	
QY	710	CTGAACATCACGACTGTGCATGATGTTTGGCTGAGACGCTCTTGGTGGAGACATGTTT	769	
Db	661	CTGAACATCACGACTGTGCATGATGTTTGGCTGAGACGCTCTTGGTGGAGACATGTTT	720	
QY	770	AATTAATCTTCTCTCTGAGCAATTTGGGGTCTTTCTGTTCACAGCCTTCTCTACAGCCTCT	829	
Db	721	AATTAATCTTCTCTCTGAGCAATTTGGGGTCTTTCTGTTCACAGCCTTCTCTACAGCCTCT	780	
QY	830	GCCATATGTGATGATCAGATGCTGCGATCTTCTGCAATGAAATCTCAGAGAG	889	
Db	781	GCCATATGTGATGATCAGATGCTGCGATCTTCTGCAATGAAATCTCAGAGAG	840	
QY	890	AAAGGAAGAGGGGCATCAAACTCATTTGTCATGCTCCGAGGACATGATCTGCTTC	949	
Db	841	AAAGGAAGAGGGGCATCAAACTCATTTGTCATGCTCCGAGGACATGATCTGCTTC	900	
QY	950	ACTCTTAGTAACCTTGTGCTGTGTGATTAATTTTGATTAAGACCAAGGCGCAGAC	1009	
Db	901	ACTCTTAGTAACCTTGTGCTGTGTGATTAATTTTGATTAAGACCAAGGCGCAGAC	960	
QY	1010	CATGTCTATGCGCTGTACATTTTGAAGCCCTGTGCTCTTACCTTTAACAGCTGATGAC	1069	
Db	961	CATGTCTATGCGCTGTACATTTTGAAGCCCTGTGCTCTTACCTTTAACAGCTGATGAC	1020	
QY	1070	CCCTTTGTCTATTACTTTGTTTCAATGATTTTCAAGGATCATGTGAAAGAAAGCGCTCTCCTT	1129	
Db	1021	CCCTTTGTCTATTACTTTGTTTCAATGATTTTCAAGGATCATGTGAAAGAAAGCGCTCTCCTT	1080	

AC ADO29874;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Human GPCR F2RL1 polynucleotide, SEQ ID NO:976.
 DE
 XX
 XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 KW cytotoxic; antiinflammatory; vasotropic; antiangiinal; antidiabetic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antihypertensive;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antidiuretic; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW gene; ss.
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO2004040000-A2.
 PN
 XX
 XX 13-MAY-2004.
 PD
 XX
 XX 09-SEP-2003; 2003WO-US028226.
 PF
 XX
 XX 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 XX (PRIM-) PRIMAL INC.
 PA
 XX
 XX Galenatis GA, Bergmann JB, Gragerov A, Hohmann J, Li F,
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
 XX
 XX MPI; 2004-390329/36.
 DR P-PSDB; ADO29311.
 XX
 XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 PT
 XX
 XX Claim 151; SEQ ID NO 976; 542pp; English.
 PS
 XX
 XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,

CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR encoding
 CC nucleic acid of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1194 BP; 264 A; 322 C; 261 G; 347 T; 0 U; 0 Other;

QY Query Match 83.4%; Score 1179.6; DB 12; Length 1194;

Best Local Similarity 99.2%; Pred. No. 0;

Matches 1185; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 50 ATGCGAGGCCCAAGCGGCGTGGCTGTGGGAGCGCCATCTGCTAGCAGCTTCTC 109
 DB 1 ATGCGGAGGCCCAAGCGGCGTGGCTGTGGGAGCGCCATCTGCTAGCAGCTTCTC 60
 QY 110 TCTGAGAGGACCACTCCAGAAACCAATATCTCTAAAGAAAGAGCCCTTATGGCT 169
 DB 61 TCTGCAAGGACCACTCCAGAAACCAATATCTCTAAAGAAAGAGCCCTTATGGCT 120
 QY 170 AAGTTGATGGACATCCCAAGTCACTGGAAAAAGAGTTACAGTTGAACAGTCTTTCT 229
 DB 121 AAGTTGATGGACATCCCAAGTCACTGGAAAAAGAGTTACAGTTGAACAGTCTTTCT 180
 QY 230 GTGATGAGTTTTCTGCACTGTCTCTGCTGAGAAAATGACCACTGTCTTCTCAATT 289
 DB 181 GTGATGAGTTTTCTGCACTGTCTCTGCTGAGAAAATGACCAAGGTCTTCTTCAATT 240
 QY 290 GTCTACAAATGTGTTCGGGTGGTTTGGCAAGTAAGGCAATGGCCCTTATGGCTTT 349
 DB 241 GTCTACAAATGTGTTCGGGTGGTTTGGCAAGTAAGGCAATGGCCCTTATGGCTTT 300
 QY 350 CTTTCCGAACCTAAGAAAGACCACTGCTGATTTATCATGAGCCATCTGACCTTGCT 409
 DB 301 CTTTCCGAACCTAAGAAAGACCACTGCTGATTTATCATGAGCCATCTGACCTTGCT 360
 QY 410 GACCTCTCTCTGTCACTGTGTTTCCCTTGAAGATTGCTTATCATGAGCCATCTG 469
 DB 361 GACCTCTCTCTGTCACTGTGTTTCCCTTGAAGATTGCTTATCATGAGCCATCTG 420
 QY 470 TGGATTTATGGGAAAGCTTTTGTAAATGCTTATTTGGCTTTTTCATGCAACATGTA 529
 DB 421 TGGATTTATGGGAAAGCTTTTGTAAATGCTTATTTGGCTTTTTCATGCAACATGTA 480
 QY 530 TGTTCATCTCTCTATGACCTGCTCAGTGTGACAGAGTATTTGGTCACTGTGAACCC 589
 DB 481 TGTTCATCTCTCTATGACCTGCTCAGTGTGACAGAGTATTTGGTCACTGTGAACCC 540
 QY 590 ATGGGGCACTCCAGAAAGGCAAACTTGCATTTGGCATTCCTGGCAATATGGCTG 649
 DB 541 ATGGGGCACTCCAGAAAGGCAAACTTGCATTTGGCATTCCTGGCAATATGGCTG 600
 QY 650 CTGACCTGCTGCTACCACTCCCTTTGTAATGTCGAAACACACATCTTCAATTCCTG 709
 DB 601 CTGATTCCTGCTGCTACCACTCCCTTTGTAATGTCGAAACACACATCTTCAATTCCTG 660
 QY 710 CTGAACATCAGCACTGTGATGTTTGGCTGAGAGCTCTTGGTGGAGACATGTTTC 769
 DB 661 CTGAACATCAGCACTGTGATGTTTGGCTGAGAGCTCTTGGTGGAGACATGTTTC 720
 QY 770 AATTACTTCTCTCTTGGCCATTTGGGATCTTTTGTGTTCCAGCTTCTCAAGCTCT 829
 DB 721 AATTACTTCTCTCTTGGCCATTTGGGATCTTTTGTGTTCCAGCTTCTCAAGCTCT 780
 QY 830 GCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 889
 DB 781 GCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
 QY 890 AAAAGGAAGAGGAGGCACTCAATGTCATGTCCTGAGGATGATGATGATGATGATG 949
 DB 841 AAAAGGAAGAGGAGGCACTCAATGTCATGTCCTGAGGATGATGATGATGATGATG 900

QY 950 ACTCTGATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1009
 Db 901 ACTCTGATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 960
 QY 1010 CATGTCTATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1069
 Db 961 CATGTCTATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1020
 QY 1070 CCCCTTCTATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1129
 Db 1021 CCCCTTCTATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1080
 QY 1130 TGCCTGATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1189
 Db 1081 TGCCTGATGACCTTCTGCTGTGATGATATTTCTGATTAAGACGAGGCGAGGC 1140
 QY 1190 AGGAAATCCAGCTCTTCACTTCAAGTTCAACCACTGTTAAGACCTCTATTGA 1243
 Db 1141 AGGAAATCCAGCTCTTCACTTCAAGTTCAACCACTGTTAAGACCTCTATTGA 1194
 RESULT 15
 AA084558 standard; DNA; 1255 BP.
 AC AA084558;
 DT 25-MAR-2003 (revised)
 DT 22-AUG-1995 (first entry)
 DE Human C140 receptor genomic DNA.
 KM G-protein-coupled receptor; G-protein; C140 receptor; 88.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 56..1197
 FT /tag = a
 PN MO9503318-A1.
 PD 02-FEB-1995.
 PF 26-JUL-1994; 94MO-US008536.
 PR 26-JUL-1993; 93US-00097938.
 PA (COR-) COR THERAPEUTICS.
 PI Scarborough RM, Sundelin J;
 DR WPI; 1995-075182/10.
 DR P-PSDB; AAR66921.
 XX New DNA encoding recombinant C140 receptor - and novel agonists and
 PT antagonists and specific antibodies with therapeutic and diagnostic
 PT applications.
 PS Disclosure; Fig 2; 57pp; English.
 CC The availability of genomic DNA encoding the mouse protease C140 receptor
 CC (see Q84557) permitted the retrieval of the corresp. human gene. A human
 CC genomic library cloned in the vector EMBL3 was screened using the entire
 CC coding region of the murine clone as a probe. The recovered human gene
 CC including the DNA sequence and the deduced AA sequence are shown in
 CC 084558 & R66921. Subsequent experiments indicated that the human C140
 CC gene is located in the same region of the long arm of chromosome number 5
 CC (3q12-5q13) as has been reported for the human thrombin receptor gene.
 CC *Updated on 25-MAR-2003 to correct PN field.)
 CC CC
 CC CC
 CC Sequence 1255 BP; 294 A; 320 C; 260 G; 381 T; 0 U; 0 Other;

Query Match 78.2%; Score 1105.8; DB 2; Length 1255;
 Best Local Similarity 99.4%; Pred. No. 0;
 Matches 1110; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 130 AGGAAATCCAGCTCTTCACTTCAAGTTCAACCACTGTTAAGACCTCTATTGA 189
 Db 139 AGGAAATCCAGCTCTTCACTTCAAGTTCAACCACTGTTAAGACCTCTATTGA 198
 QY 190 CGTCACATGAGAAAGAGTTACATTTGAAACAGCTTTCTGAGAGAGAGTTTCTGATC 249
 Db 199 CGTCACATGAGAAAGAGTTACATTTGAAACAGCTTTCTGAGAGAGAGTTTCTGATC 258
 QY 250 TGTCTGCTGAGAAAGAGTTACATTTGAAACAGCTTTCTGAGAGAGAGTTTCTGATC 309
 Db 259 TGTCTGCTGAGAAAGAGTTACATTTGAAACAGCTTTCTGAGAGAGAGTTTCTGATC 318
 QY 310 GGTGGGTTTCCAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAG 369
 Db 319 GGTGGGTTTCCAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAGTAAAGGAG 378
 QY 370 GCAACCTGCTGATTTTCAATGAGCAATCTGAGCTTGGAGTAAAGTAAAGTAAAG 429
 Db 379 GCAACCTGCTGATTTTCAATGAGCAATCTGAGCTTGGAGTAAAGTAAAGTAAAG 438
 QY 430 GTTCCCTTGAAGATTTGCTATGACATATGAGCAACATGATTTTATGAGGAGTCT 489
 Db 439 GTTCCCTTGAAGATTTGCTATGACATATGAGCAACATGATTTTATGAGGAGTCT 498
 QY 490 TTGTAATGCTTATTTGCTTTTCTATGAGCAATGATGATGATGATGATGATGAT 549
 Db 499 TTGTAATGCTTATTTGCTTTTCTATGAGCAATGATGATGATGATGATGATGAT 558
 QY 550 CTGCTGAGTGTGAGAGAGTATTTGAGTATGATGATGATGATGATGATGATGAT 609
 Db 559 CTGCTGAGTGTGAGAGAGTATTTGAGTATGATGATGATGATGATGATGATGAT 618
 QY 610 GGCAGACATTTGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 669
 Db 619 GGCAGACATTTGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 678
 QY 670 CCCCTTGTATGCTGAGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 729
 Db 679 CCCCTTGTATGCTGAGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 738
 QY 730 TGAATGTTTCCCTGAGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 789
 Db 739 TGAATGTTTCCCTGAGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 798
 QY 790 CATTTGGGCTTTCTGATTTCCAGAGCTTTCTCAAGAGCTTTGCTATGATGATGAT 849
 Db 799 CATTTGGGCTTTCTGATTTCCAGAGCTTTCTCAAGAGCTTTGCTATGATGATGAT 858
 QY 850 AATGCTGATCTTCTGAGTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 909
 Db 859 AATGCTGATCTTCTGAGTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 918
 QY 910 ACTCATTTGATCTGCTGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 969
 Db 919 ACTCATTTGATCTGCTGAGAGTATTTGAGTATTTGAGTATTTGAGTATTTGAG 978
 QY 970 TGTGAGTATTTCTGATTTTCAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1029
 Db 979 TGTGAGTATTTCTGATTTTCAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1038
 QY 1030 TGTAGCCTTCTGCTCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1089
 Db 1039 TGTAGCCTTCTGCTCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1098
 QY 1090 TTGACATGATTTTCAAGAGTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1149
 Db 1099 TTGACATGATTTTCAAGAGTATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1158
 QY 1150 AATGAGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1209

Db	1159	AAAGCAGATGCAGTAATCCCTCAGCTCAAGAAACACTCCAGGAAATCCAGCTTACTC	1218
Qy	1210	TTCAAGTTCACCACTGTAAAGCCTCCTATTGAGTT	1246
Db	1219	TTCAAGTTCACCACTGTTAAGACTTCTATTGAGTT	1255

Search completed: March 21, 2005, 18:18:56
Job time : 830.407 secs

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MRSPPSAAMLGAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
DB 1 MRSPPSAAMLGAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
QY 61 VDEFSASVLAGKLTVPPIVYTVPAVGLPSNGMALWVLPFRKKKHPAVIYMANLALA 120
DB 61 VDEFSASVLAGKLTVPPIVYTVPAVGLPSNGMALWVLPFRKKKHPAVIYMANLALA 120
QY 121 DLLSVMPFLKIAVHGHNNWYIGBALCNVLIGFFYGNMYCSILFMTCLSVORRWYIYVNP 180
DB 121 DLLSVMPFLKIAVHGHNNWYIGBALCNVLIGFFYGNMYCSILFMTCLSVORRWYIYVNP 180
QY 181 MGHSRKKNIAIGISLAIWMLTLVTIPLYVVKQITFIPALNITTCGDVLPBQLLVGDMF 240
DB 181 MGHSRKKNIAIGISLAIWMLTLVTIPLYVVKQITFIPALNITTCGDVLPBQLLVGDMF 240
QY 241 NYFLSLAIGVFLPPAPLTSAYVLMRLRSSAMDBNSKKRRRAIKLIVTVLGMVLICF 300
DB 241 NYFLSLAIGVFLPPAPLTSAYVLMRLRSSAMDBNSKKRRRAIKLIVTVLGMVLICF 300
QY 301 TSPNLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNAL 360
DB 301 TSPNLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNAL 360
QY 361 CRSVRTVKQOVPLTSKGRSSSYSSSTTVKTSY 397
DB 361 CRSVRTVKQOVPLTSKGRSSSYSSSTTVKTSY 397

```

RESULT 2
AAM01955
ID AAM01955 standard; protein; 397 AA.

AC AAM01955;

DT 02-APR-1997 (first entry)

XX Human C140 receptor.

XX C140 receptor; G-protein linked; coupled; seven pass; agonist;
XX antagonist; hypertension; hypotension; blood pressure.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..27
FT /note="the signal peptide differs from that encoded by a
FT genomic DNA sequence for this receptor (see AAM01953),
FT the signal sequence given here is believed to be the
FT correct sequence"
FT 28..397
FT Protein /note="mature protein"

XX MO9623225-A1.

XX 01-AUG-1996.

XX 25-JAN-1996; 96MO-US001179.

XX 25-JAN-1995; 95US-00390301.

XX (CORT-) COR THERAPEUTICS INC.

XX Sundelin J, Scarborough RM;

XX WPI, 1996-362813/36.

XX DR N-PSDB; AAT32039.

XX Vector for expression C140 cell surface receptor in host cell - useful to
XX identify C140 agonist and antagonists, which are antihypertensives and
XX elevators of blood pressure, respectively.

PS Example 5; Fig 11A-B; 60pp; English.
XX AAM01955 represents the human C140 receptor (C140R). DNA encoding C140R
CC may be engineered so as to allow the recombinant expression of C140R in a
CC suitable host cell, i.e. by removing the native expression-control
CC sequences and replacing them with control sequences operable in the host.
CC Such a recombinant receptor can be expressed on the surface of oocytes,
CC this provides a good assay system for identifying agonists/antagonists of
CC C140R. The C140 receptor is a G-protein linked receptor and a member of
CC the "seven-pass" transmembrane receptor superfamily (peptide chain of the
CC receptor passes through the cell membrane seven times, producing seven
CC transmembrane regions within the receptor molecule). The C140 receptor is
CC involved in controlling blood pressure. C140 antagonists (see AAM01942,
CC an increase in blood pressure and are therefore useful in pharmaceuticals
CC for the treatment of hypertension (low blood pressure). Conversely
CC agonists (see AAM01944-W01941) of C140 are useful in pharmaceuticals for
CC the treatment of hypertension (high blood pressure)

SQ Sequence 397 AA;

Query Match 99.6%; Score 2023; DB 2; Length 397;

Best Local Similarity 99.7%; Pred. No. 1..le-210;

Matches 396; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1 MRSPPSAAMLGAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
DB 1 MRSPPSAAMLGAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGTSHTGKGVTVETVS 60
QY 61 VDEFSASVLAGKLTVPPIVYTVPAVGLPSNGMALWVLPFRKKKHPAVIYMANLALA 120
DB 61 VDEFSASVLAGKLTVPPIVYTVPAVGLPSNGMALWVLPFRKKKHPAVIYMANLALA 120
QY 121 DLLSVMPFLKIAVHGHNNWYIGBALCNVLIGFFYGNMYCSILFMTCLSVORRWYIYVNP 180
DB 121 DLLSVMPFLKIAVHGHNNWYIGBALCNVLIGFFYGNMYCSILFMTCLSVORRWYIYVNP 180
QY 181 MGHSRKKNIAIGISLAIWMLTLVTIPLYVVKQITFIPALNITTCGDVLPBQLLVGDMF 240
DB 181 MGHSRKKNIAIGISLAIWMLTLVTIPLYVVKQITFIPALNITTCGDVLPBQLLVGDMF 240
QY 241 NYFLSLAIGVFLPPAPLTSAYVLMRLRSSAMDBNSKKRRRAIKLIVTVLGMVLICF 300
DB 241 NYFLSLAIGVFLPPAPLTSAYVLMRLRSSAMDBNSKKRRRAIKLIVTVLGMVLICF 300
QY 301 TSPNLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNAL 360
DB 301 TSPNLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNAL 360
QY 361 CRSVRTVKQOVPLTSKGRSSSYSSSTTVKTSY 397
DB 361 CRSVRTVKQOVPLTSKGRSSSYSSSTTVKTSY 397

```

RESULT 3

AAB35641
ID AAB35641 standard; protein; 397 AA.

XX AAB35641;

XX 19-FEB-2001 (first entry)

XX Human PAR-2 protein.

XX PAR-2; protease activated receptor-2; ECL-2; inflammatory disease;
XX asthma; chronic obstructive pulmonary; arthritis; inflammatory bowel;
XX psoriasis; eczema; multiple sclerosis.

XX Homo sapiens.

XX MO200063371-A1.

XX 26-OCT-2000.

Db 241 NYFLSLAIGVFLPAPLTAASAVYLMIRLSSAMDESEKRRRAIKLIVTLAMYLICF 300
QY 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCSTLNSCIDPFYVYVSHDFRDHAKNALL 360
Db 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCSTLNSCIDPFYVYVSHDFRDHAKNALL 360
QY 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSSTTVKTSY 397
Db 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSSTTVKTSY 397

RESULT 5
ABG73508
ID ABG73508 standard; protein; 397 AA.
XX
XX ABG73508;
AC
XX
XX 14-FEB-2003 (first entry)
XX
XX
DE Human par2 protein SEQ ID 39.
XX
XX
XX G-protein coupled receptor; HGPBRMY1, HGPBRMY2; immunosuppressive;
XX
XX
XX vaccinate; neuroprotective; antiinflammatory; cyostatic; vulnerrary;
XX
XX
XX haematopoietic; pulmonary; gastrointestinal; proliferation; cell cycle;
XX
XX
XX birth defect; aberrant phosphorylation; acute phase response; receptor;
XX
XX
XX signal transduction; hyperimmune activity; inflammatory; hypercongenital;
XX
XX
XX necrotic lesion; wound; organ transplant rejection.
XX
XX
XX Homo sapiens.
XX
XX
XX MO200268591-A2.
XX
XX
XX 06-SEP-2002.
XX
XX
XX 22-FEB-2002; 2002WO-US005281.
XX
XX
XX 23-FEB-2001; 2001US-0270792P.
XX
XX
XX 23-FEB-2001; 2001US-0270793P.
XX
XX
XX 06-JUN-2001; 2001US-0296427P.
XX
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX
XX Feder J, Ramathan C, Nelson T, Muntier G, Cacace A, Barber L;
XX
XX
XX Kornacker M, Bol D;
XX
XX
XX MPI; 2003-058304/05.
XX
XX
XX New human HGPBRMY1 or HGPBRMY2 polynucleotide and polypeptide, useful
XX
XX
XX preventing, treating or ameliorating a disorder e.g., wound,
XX
XX
XX cardiovascular disorder or transplant rejection.
XX
XX
XX Disclosure; Fig 4; 316pp; English.
XX
XX
XX This invention describes the novel human G-protein coupled receptors
XX
XX
XX (GPCR's), HGPBRMY1 or HGPBRMY2 which have immunosuppressive, cardiant,
XX
XX
XX neuroprotective, antiinflammatory, cyostatic and vulnerrary activity and
XX
XX
XX can be used in vaccines or for gene therapy. Pharmaceutical compositions
XX
XX
XX comprising HGPBRMY1 or HGPBRMY2 polypeptides or their agonists or
XX
XX
XX antagonists or modulators, or a HGPBRMY1- or HGPBRMY2-specific antibody
XX
XX
XX are useful for preventing, treating or ameliorating a medical condition
XX
XX
XX comprising autoimmune, cardiovascular, neural, reproductive,
XX
XX
XX haematopoietic, pulmonary, gastrointestinal or proliferating disorder, a
XX
XX
XX cell cycle or birth defect, a disorder related to aberrant
XX
XX
XX phosphorylation, acute phase responses or signal transduction or to
XX
XX
XX hyperimmune activity, an inflammatory or hypercongenital condition, a
XX
XX
XX necrotic lesion, a wound, organ transplant rejection or a condition
XX
XX
XX related to organ transplant rejection. This sequence represents a G-
XX
XX
XX protein coupled receptor associated with the human HGPBRMY proteins
XX
XX
XX described in the disclosure of the invention
XX
XX
XX Sequence 397 AA;
XX

Query Match 98.6%; Score 2003; DB 6; Length 397;
Best Local Similarity 98.7%; Pred. No. 1.7e-208;
Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 MNSPSAAMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
Db 1 MNSPSAAMLLGAAILLAASLSCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
QY 61 VDEFSASVLTGKLTIVFLPIVTVIVPAVGLPNSGMALWFLPRTKKGPAVIYMANLALA 120
Db 61 VDEFSASVLTGKLTIVFLPIVTVIVPAVGLPNSGMALWFLPRTKKGPAVIYMANLALA 120
QY 121 DLLSVIWPFLKIAVHIGNNMITYGALCNVLIGFPYNNYCSILFWTCLSVORRYVYVNP 180
Db 121 DLLSVIWPFLKIAVHIGNNMITYGALCNVLIGFPYNNYCSILFWTCLSVORRYVYVNP 180
QY 181 MGHSRKKANIAIGISLALWTLTLVTIPLYVVKQITFIIPALNITTCDDVLPQDLVGDNF 240
Db 181 MGHSRKKANIAIGISLALWTLTLVTIPLYVVKQITFIIPALNITTCDDVLPQDLVGDNF 240
QY 241 NYFLSLAIGVFLPAPLTAASAVYLMIRLSSAMDESEKRRRAIKLIVTLAMYLICF 300
Db 241 NYFLSLAIGVFLPAPLTAASAVYLMIRLSSAMDESEKRRRAIKLIVTLAMYLICF 300
QY 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCSTLNSCIDPFYVYVSHDFRDHAKNALL 360
Db 301 TTSNLLLVVHYFLIKSQGSHVYALYVALCSTLNSCIDPFYVYVSHDFRDHAKNALL 360
QY 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSSTTVKTSY 397
Db 361 CRSVRTVKOMQVPLTSKSKSRKSSSYSSSSTTVKTSY 397

RESULT 6
ADE62812
ID ADE62812 standard; protein; 397 AA.
XX
XX
XX ADE62812;
XX
XX
XX 29-JUN-2004 (first entry)
XX
XX
XX Human Protein P55085, SEQ ID NO 8745.
XX
XX
XX Human; pain; neuronal tissue; gene therapy;
XX
XX
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX
XX
XX spared nerve injury; SNr; Chung.
XX
XX
XX Homo sapiens.
XX
XX
XX MO2003016475-A2.
XX
XX
XX 27-FEB-2003.
XX
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX
XX 14-AUG-2001; 2001US-0312147P.
XX
XX
XX 01-NOV-2001; 2001US-0346382P.
XX
XX
XX 26-NOV-2001; 2001US-0333347P.
XX
XX
XX (GENO) GEN HOSPITAL CORP.
XX
XX
XX (FARB) BAYER AG.
XX
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX
XX MPI; 2003-268312/26.
XX
XX
XX GENBANK; P55085.
XX
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX
XX
XX preparing a medicament for treating pain in an animal.
XX
XX
XX Claim 1; Page; 1017pp; English.
XX

XX Sequence 397 AA;
 SQ Query Match 98.6%; Score 2003; DB 8; Length 397;
 Best local similarity 98.7%; Pred. No. 1.7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 DB 1 MRSPSAAMLLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 QY 61 VDEFSASVLAGLTTVPLPIVTVTVFAVGLPSNGMALMWFLFRTKKKHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGLTTVPLPIVTVTVFAVGLPSNGMALMWFLFRTKKKHPAVIYMANIALA 120
 QY 121 DLLSVTFPLKIAHYHIGNNWIYGEALCNVLIGFPGNNYCSILPMTCLSVGRWYIYNP 180
 DB 121 DLLSVTFPLKIAHYHIGNNWIYGEALCNVLIGFPGNNYCSILPMTCLSVGRWYIYNP 180
 QY 181 MGHSRKKANIAIGISLAIWLLTLVTIPLVYVKQTIPIPALNITTCDDVLPEQLLVGDMF 240
 DB 181 MGHSRKKANIAIGISLAIWLLTLVTIPLVYVKQTIPIPALNITTCDDVLPEQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPAPFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVLGMYLICF 300
 DB 241 NYFLSLAIGVFLPAPFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVLGMYLICF 300
 QY 301 TSPNLLLVHYHFLIKSQGSHVYALYVALCSTLNSCIDPFIYVYFVSHDFRDHAKNAL 360
 DB 301 TSPNLLLVHYHFLIKSQGSHVYALYVALCSTLNSCIDPFIYVYFVSHDFRDHAKNAL 360
 QY 361 CRSVRTVKOMQVPLTSKHSKRSSSYSSSTTVKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKHSKRSSSYSSSTTVKTSY 397

RESULT 8
 ADST74020
 ID ADST74020 standard; protein; 397 AA.
 XX
 AC ADST74020;
 DT 16-DEC-2004 (first entry)
 DE Human G-protein coupled proteinase activated receptor 2 (PAR2).
 KW Human; proteinase activated receptor 2; PAR2; G-protein coupled receptor;
 KW receptor; cardiant; neuroprotective; nephrotropic; respiratory-gen.;
 KW gastrointestinal-gen.; gene therapy.
 OS Homo sapiens.
 XX
 PN MO2004080373-A2.
 PD 23-SEP-2004.
 PF 26-FEB-2004; 2004MO-EP001896.
 PR 11-MAR-2003; 2003EP-00004980.
 PA (FARB) BAYER HEALTHCARE AG.
 PI Golz S, Brueggemeier U, Summer H;
 DR MPI: 2004-677358/66.
 DR N-PSDB; ADST74019.
 XX
 XX Screening for therapeutic agents for treating e.g., cardiovascular
 PT diseases by contacting a test compound with a proteinase activated
 PT receptor 2 (PAR2) polypeptide or polynucleotide and detecting binding of
 PT the test compound.
 PS Disclosure; SEQ ID NO 2, 121pp; English.

XX The present sequence is that of human G-protein coupled proteinase
 CC activated receptor 2 (PAR2). PAR2 is an antiinflammatory receptor in the
 CC colon and may also play a role in the airway, regulating sodium ion
 CC absorption and anion secretion. The invention relates to novel disease
 CC associations of PAR2 polypeptides and polynucleotides. It also relates to
 CC novel methods of screening for therapeutic agents for the treatment of
 CC cardiovascular disorders, gastrointestinal and liver diseases,
 CC neurological disorders, urological disorders, haematological diseases and
 CC respiratory diseases in a mammal. Suitable therapeutic agents include a
 CC small molecule, an RNA molecule, an antisense oligonucleotide, a
 CC polypeptide, an antibody or a ribozyme. The invention also provides
 CC pharmaceutical compositions for the treatment of diseases and disorders
 CC associated with PAR2 comprising a PAR2 polypeptide, PAR2 polynucleotide
 CC or a regulator or modulator of PAR2 activity. Methods of diagnosing these
 CC diseases and disorders involve determining the amount of PAR2
 CC polynucleotide in a sample.

XX Sequence 397 AA;
 SQ Query Match 98.6%; Score 2003; DB 8; Length 397;
 Best local similarity 98.7%; Pred. No. 1.7e-208;
 Matches 392; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 MRSPSAAMLLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 DB 1 MRSPSAAMLLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 QY 61 VDEFSASVLAGLTTVPLPIVTVTVFAVGLPSNGMALMWFLFRTKKKHPAVIYMANIALA 120
 DB 61 VDEFSASVLAGLTTVPLPIVTVTVFAVGLPSNGMALMWFLFRTKKKHPAVIYMANIALA 120
 QY 121 DLLSVTFPLKIAHYHIGNNWIYGEALCNVLIGFPGNNYCSILPMTCLSVGRWYIYNP 180
 DB 121 DLLSVTFPLKIAHYHIGNNWIYGEALCNVLIGFPGNNYCSILPMTCLSVGRWYIYNP 180
 QY 181 MGHSRKKANIAIGISLAIWLLTLVTIPLVYVKQTIPIPALNITTCDDVLPEQLLVGDMF 240
 DB 181 MGHSRKKANIAIGISLAIWLLTLVTIPLVYVKQTIPIPALNITTCDDVLPEQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPAPFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVLGMYLICF 300
 DB 241 NYFLSLAIGVFLPAPFLTASAVYLMIRLSSAMDENSEKKRAIKLIVTVLGMYLICF 300
 QY 301 TSPNLLLVHYHFLIKSQGSHVYALYVALCSTLNSCIDPFIYVYFVSHDFRDHAKNAL 360
 DB 301 TSPNLLLVHYHFLIKSQGSHVYALYVALCSTLNSCIDPFIYVYFVSHDFRDHAKNAL 360
 QY 361 CRSVRTVKOMQVPLTSKHSKRSSSYSSSTTVKTSY 397
 DB 361 CRSVRTVKOMQVPLTSKHSKRSSSYSSSTTVKTSY 397

RESULT 9
 ADL61221
 ID ADL61221 standard; protein; 397 AA.
 XX
 AC ADL61221;
 DT 03-JUN-2004 (first entry)
 DE Human coagulation factor II (thrombin) receptor-like 1 protein.
 KW predictor set; protein tyrosine kinase; cytosolic; antiangiogenic;
 KW vasotropic; vulnerary; pharmacogenomic; drug sensitivity; breast cancer;
 KW hypervascular disease; angiogenesis; wound healing scar; human;
 KW biomarker; coagulation factor II receptor-like I; thrombin; receptor.
 OS Homo sapiens.
 XX
 XX MO2004020583-A2.
 PN 11-MAR-2004.
 PD

XX 26-AUG-2003; 2003WO-US026491.
 XX
 XX 27-AUG-2002; 2002US-0406385P.
 XX
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 XX Huang F, Han X, Reeves KA, Amler L, Fairchild CR, Lee FY;
 XX Shaw P;
 XX WPI; 2004-239171/22.
 XX N-PSDB; ADL61084.
 XX
 XX New predictor sets with a plurality of polynucleotides and/or
 XX polypeptides whose expression pattern predicts cell response to a
 XX compound that modulates protein tyrosine kinase activity, useful in
 XX treating breast cancer.
 XX
 XX Claim 9; SEQ ID NO 145; 649pp; English.
 XX
 XX The invention relates to a novel predictor set comprising a plurality of
 XX polynucleotides and/or polypeptides whose expression pattern is
 XX predictive of the response of cells to treatment with a compound that
 XX modulates protein tyrosine kinase activity or members of the protein
 XX tyrosine kinase pathway. The molecules of the invention demonstrate
 XX cytosolic, angiogenic, vasotropic and vulnary activities and may
 XX be useful in the field of pharmacogenomics, in particular for determining
 XX drug sensitivity and in treating breast cancer, hypervascular diseases,
 XX angiogenesis and scars in wound healing. The current sequence is that of
 XX a human protein tyrosine kinase biomarker protein of the invention.
 XX
 XX Sequence 397 AA;
 XX
 XX Query Match 98.4%; Score 1998; DB 8; Length 397;
 XX Best Local Similarity 98.5%; Pred. No. 5.9e-208;
 XX Matches 391; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 XX
 XX 1 MNSPSAAMTLLGAAILLAASLSCSGTIGTRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX 1 MNSPSAAMTLLGAAILLAASLSCSGTIGTRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX
 XX RESULT 10
 XX ABB81907
 XX ID ABB81907 standard; protein; 397 AA.
 XX
 XX * ABB81907;
 XX AC
 XX XX
 XX DT 04-MAR-2003 (first entry)

XX DE Human proteinase-activated receptor 2 protein SEQ ID NO:300.
 XX
 XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 XX KW G protein-coupled receptor modulator; antibody; immune-related disease;
 XX KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 XX KW immunological-related cell proliferative disease; autoimmune disease;
 XX KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 XX KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 XX KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 XX KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 XX KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 XX KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 XX KW ulcer.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200261087-A2.
 XX
 XX PD 08-AUG-2002.
 XX
 XX PF 19-DEC-2001; 2001WO-US050107.
 XX
 XX PR 19-DEC-2000; 2000US-0257144P.
 XX
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX
 XX PI Burner GC, Roush CL, Brown JP;
 XX
 XX WPI; 2003-046718/04.
 XX N-PSDB; AB242755.
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 XX (GPCR), useful for diagnosing and designing drugs for treating conditions
 XX in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 XX autoimmune diseases.
 XX
 XX Disclosure; Fig 1; 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 XX any one of 1601 sequences (see ABB82619 to ABB82619) of 12-24 amino
 XX acids. Also described: (1) an assay for the detection of a particular G
 XX protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 XX and (2) an isolated antibody having high specificity and high affinity or
 XX avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 XX gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 XX antibody against a particular GPCR, and in the production of specific
 XX antibodies. The peptides and antibodies are also useful for detecting the
 XX presence or absence of corresponding GPCRs. The antigenic peptides for
 XX GPCRs and antibodies are useful for diagnosing and designing drugs for
 XX treating immune-related diseases, growth-related diseases, cell
 XX regeneration-related disease, immunological-related cell proliferative
 XX diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 XX atherosclerosis, bacterial, fungal, protozoan or viral infections,
 XX osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 XX inflammation, allergies, Crohn's disease, diabetes, graft versus host
 XX disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 XX anxiety, depression, schizophrenia, dementia, mental retardation, memory
 XX loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 XX hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 XX any other disorder in which GPCRs are involved. The antibodies may be
 XX used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 XX GPCR proteins given in ABB81675 to ABB82018, which are used in the
 XX exemplification of the present invention
 XX
 XX Sequence 397 AA;
 XX
 XX Query Match 98.3%; Score 1997; DB 6; Length 397;
 XX Best Local Similarity 98.5%; Pred. No. 7.6e-208;
 XX Matches 391; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 XX
 XX 1 MNSPSAAMTLLGAAILLAASLSCSGTIGTRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX 1 MNSPSAAMTLLGAAILLAASLSCSGTIGTRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX 61 VDEFSASVLAGKLTTPVPIVTVAVGLPSNGMALMVEFPFKKKHPAVIYMANLALA 120
 XX
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX 121 DLISVIMPLKATIAHIGNNNIYGBALCNVLIQPFYGNMTCSILFMTCLSVQRVWTVNP 180
 XX
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX 181 MGRSRKKAIAIGISLAIWLTLLNTPIYVVKQTFIPALNTTTCGDDVPEGLVGDMP 240
 XX
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX 241 NYFLSLAIGVFLPAPFLTASAVVLMIRLSSAMDNSEKKRRAIKLITVLAGMYLICP 300
 XX
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX 301 TPNALLLVHYFLIKSQGSHVVALYIVACLSLNSCIDPFYVYSHDFRDHAKNAL 360
 XX
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX 361 CRSVTRVKOMQVPLTSKGRSSKSSSYSSSTTWTCTY 397
 XX

KM retinal neovascularisation syndrome; scarring; uterine fibroid;
 KM detection; diagnosis; prognosis; drug screening; drug targeting;
 KM wound healing; contraception; cytostatic; cardiac; immunomodulatory;
 KM vulnerrary; gene therapy; vaccine.

OS Homo sapiens.

XX MO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002MO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

PR 21-NOV-2001; 2001US-0332464P.

PR 29-NOV-2001; 2001US-0334393P.

PR 03-DEC-2001; 2001US-0335394P.

PR 14-DEC-2001; 2001US-0340376P.

PR 08-JAN-2002; 2002US-0347211P.

PR 10-JAN-2002; 2002US-0347349P.

PR 08-FEB-2002; 2002US-0355250P.

PR 13-FEB-2002; 2002US-0356714P.

PR 20-FEB-2002; 2002US-0359077P.

PR 29-MAR-2002; 2002US-0368809P.

PR 04-APR-2002; 2002US-0370110P.

PR 12-APR-2002; 2002US-0372246P.

PR 05-JUN-2002; 2002US-0386614P.

PR 16-JUL-2002; 2002US-0396839P.

PR 22-JUL-2002; 2002US-0397755P.

PR 22-JUL-2002; 2002US-0397845P.

PR 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D, Aziz N, Ginsburg WM, Glah KC, Glynn R, Hevezi PA;

PI Mack DH, Murray R, Watson SR, Wilson KE, Zlocznik A;

XX WPI; 2003-468649/44.

XX N-PSDB; ADN39780.

XX Determining the presence or absence of a pathological cell in a patient,

XX useful for diagnosing, prognosing or treating cancer, comprises detecting

XX a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C367; 1385bp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

XX whose expression is upregulated or downregulated in specific cancers or

XX other diseases such as angiogenic or fibrotic disorders, and to methods

XX of determining the presence or absence of a pathological cell in a

XX patient by detecting a nucleic acid at least 80% identical to those of

XX the invention or by detecting a polypeptide of the invention. The

XX invention also relates to expression vectors and host cells comprising a

XX nucleic acid of the invention; antibodies which specifically bind a

XX polypeptide of the invention; use of such antibodies for drug targeting;

XX and methods of screening for modulators of activity or expression of the

XX polypeptides and nucleic acids. The nucleic acids, polypeptides,

XX antibodies and methods are useful for diagnosing, prognosing and treating

XX cancer and other conditions such as psoriasis, ischemia, heart disease,

XX atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

XX neovascularization syndromes, scarring and uterine fibroids. They may

XX also be useful in wound healing and in contraception. The present

XX sequence represents a polypeptide of the invention.

XX Sequence 397 AA;

XX Query Match 98.3%; Score 1997; DB 7; Length 397;

XX Best Local Similarity 98.5%; Pred. No. 7.6e-208; Indels 0; Gaps 0;

XX Matches 391; Conservative 0; Mismatches 6;

XX 1 MSPPSAAMLGAAILLAASLSCGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVPS 60

XX 1 MSPPSAAMLGAAILLAASLSCGTTGTRRSKGRSLGKVDGTSHTGKGVTVETVPS 60

QY VDEFSASVLAGKLTTFVFLPIVTTIVPAVGLPSNGMALWVLPRTKKGPVAVIWMALALA 120

DB 61 VDEFSASVLTGKLTTFVFLPIVTTIVPAVGLPSNGMALWVLPRTKKGPVAVIWMALALA 120

QY 121 DLLSVIWPFLKIAVYHIGNNMVIGBALCNVLIGFYGMVCSILFMTCLSVGRVWVIVNP 180

DB 121 DLLSVIWPFLKIAVYHIGNNMVIGBALCNVLIGFYGMVCSILFMTCLSVGRVWVIVNP 180

QY 181 MGRSRKKAIAIGISLAIVLTLVITPLVYVQGITFIPALNITTCGDVLPBQLVGDMP 240

DB 181 MGRSRKKAIAIGISLAIVLTLVITPLVYVQGITFIPALNITTCGDVLPBQLVGDMP 240

QY 241 NYPLSLAIGVFLPAPFLTASAVYLMIRLSSAMDSSEKGRRAIKLIVTVGMYLICF 300

DB 241 NYPLSLAIGVFLPAPFLTASAVYLMIRLSSAMDSSEKGRRAIKLIVTVGMYLICF 300

QY 301 TPSNLLLVVHYFLIKSGQSHVVALYIVLCLSTLNSCIDPFYVYVSHDFRDHAKNAL 360

DB 301 TPSNLLLVVHYFLIKSGQSHVVALYIVLCLSTLNSCIDPFYVYVSHDFRDHAKNAL 360

QY 361 CRSVRTVKQVQVPLTSKGRSRKSSSYSSSTTVKTSY 397

DB 361 CRSVRTVKQVQVPLTSKGRSRKSSSYSSSTTVKTSY 397

XX RESULT 13

XX ADR46675

XX ID ADR46675 standard; protein; 397 AA.

XX AC ADR46675;

XX DT 18-NOV-2004 (first entry)

XX DE Cancer-associated protein, SEQ ID 88.

XX KM Cytostatic; Gene Therapy; cancer; human.

XX OS Homo sapiens.

XX PN WO2004073657-A2.

XX PD 02-SEP-2004.

XX PF 19-FEB-2004; 2004MO-US005455.

XX PR 19-FEB-2003; 2003US-0448784P.

XX PA (PROT-) PROTEIN DESIGN LABS INC.

XX PI Aziz N, Glah KC, Wilson KE, Zlocznik A;

XX WPI; 2004-652787/63.

XX N-PSDB; ADR46617.

XX Detecting a pathological cell in a patient for diagnosing or treating

XX cancer by detecting in a biological sample from the patient genes whose

XX expression are up-regulated or down-regulated in specific cancers.

XX Claim 1; SEQ ID NO 88; 375bp; English.

XX The present invention relates to a method for detecting cancer in a

XX patient. The method comprises detecting in a biological sample from the

XX patient a nucleotide or protein sequence comprising a sequence that is at

XX least 80% identical to a nucleotide sequence (ADR46588-ADR46645) or

XX protein sequence (ADR46646-ADR46703). The method is useful for detecting

XX cancer for preparing a composition for diagnosing or treating cancer.

XX Sequence 397 AA;

XX Query Match 98.3%; Score 1997; DB 8; Length 397;

XX Best Local Similarity 98.5%; Pred. No. 7.6e-208; Indels 0; Gaps 0;

XX Matches 391; Conservative 0; Mismatches 6;

QY 1 MESPSPAMLLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 CC 1 MESPSPAMLLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 XX 1 MESPSPAMLLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 SQ Sequence 394 AA;
 Query Match 96.8%; Score 1965.5; DB 2; Length 394;
 Best Local Similarity 97.7%; Pred. No. 2e-204;
 Matches 388; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 QY 61 VDEFSASVLAGKLTTFPLPIVTVTVFPAVGLPSNGMALWVFLFRTKKKHPAVIYMANLALA 120
 DB 61 VDEFSASVLAGKLTTFPLPIVTVTVFPAVGLPSNGMALWVFLFRTKKKHPAVIYMANLALA 120
 QY 121 DLSVTFMPLKTAHYHNGNMYIGDALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 DB 121 DLSVTFMPLKTAHYHNGNMYIGDALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 QY 181 MGHRRKANIAGISLAIMLLTLVTIPLYVVKQTFIFPALNITTCCHDVLPBQLLVGDMF 240
 DB 181 MGHRRKANIAGISLAIMLLTLVTIPLYVVKQTFIFPALNITTCCHDVLPBQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 300
 DB 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 300
 QY 301 TSENLLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNALL 360
 DB 301 TSENLLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNALL 360
 QY 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 DB 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 RESULT 14
 AAM51408
 ID AAM51408 standard; protein; 394 AA.
 AC AAM51408;
 XX 12-OCT-1998 (first entry)
 DT 12-OCT-1998 (first entry)
 XX Human protease-activated receptor 2 (PAR2).
 DE Human protease-activated receptor 2 (PAR2).
 XX Protease-activated receptor 2; PAR2; PAR3; thrombin receptor; human.
 KM Homo sapiens.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Cleavage-site 36..37
 FT /note="thrombin cleavage site"
 XX MO9818456-A1.
 PN 07-MAY-1998.
 XX 29-OCT-1997; 97MO-US019732.
 PF 30-OCT-1996; 96US-00742440.
 PR (REGC) UNIV CALIFORNIA.
 XX Coughlin SR, Ishihara H, Connolly A;
 PI WPI, 1998-271905/24.
 DR DNA encoding protease-activated receptor 3 - for detection of specific
 XX agonists and antagonists, potentially useful for treating e.g.
 PT thrombosis, atherosclerosis, inflammation etc.
 XX Example 1; Page 43-44; 74pp; English.
 XX This polypeptide comprises human protease-activated receptor 2 (PAR2).
 CC The physiological activator of PAR2 remains unknown; it is not activated
 CC by thrombin. The invention relates to novel mouse and human PAR3 (see
 CC AAM51405-06) that show homology to PAR2 and which are specific receptors
 CC for thrombin. They can be used to screen for specific agonists and

CC antagonists of thrombin useful e.g. for treating atherosclerosis,
 CC thrombosis and inflammation
 XX
 SQ Sequence 394 AA;
 Query Match 96.8%; Score 1965.5; DB 2; Length 394;
 Best Local Similarity 97.7%; Pred. No. 2e-204;
 Matches 388; Conservative 0; Mismatches 6; Indels 3; Gaps 1;
 QY 1 MESPSPAMLLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 DB 1 MESPSPAMLLGAAILLAASLSCSGTIGQTNRSSKGRSLIGKVDGSHVTKGVTVETVS 60
 QY 61 VDEFSASVLAGKLTTFPLPIVTVTVFPAVGLPSNGMALWVFLFRTKKKHPAVIYMANLALA 120
 DB 61 VDEFSASVLAGKLTTFPLPIVTVTVFPAVGLPSNGMALWVFLFRTKKKHPAVIYMANLALA 120
 QY 121 DLSVTFMPLKTAHYHNGNMYIGDALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 DB 121 DLSVTFMPLKTAHYHNGNMYIGDALCNVLIGFFGNMYCSILFMTCLSVORWYVNP 180
 QY 181 MGHRRKANIAGISLAIMLLTLVTIPLYVVKQTFIFPALNITTCCHDVLPBQLLVGDMF 240
 DB 181 MGHRRKANIAGISLAIMLLTLVTIPLYVVKQTFIFPALNITTCCHDVLPBQLLVGDMF 240
 QY 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 300
 DB 241 NYFLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 300
 QY 240 --FLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 297
 DB 240 --FLSLAIGVFLPPAFLTASAVYLMIRLSSAMDNSSEKRRRAIKLIVTVLGMFLICF 297
 QY 301 TSENLLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNALL 360
 DB 298 TSENLLLVHYHFLIKSGQSHVYALYVALCLSTNSCIDPFYVYFVSHDFRDHAKNALL 357
 QY 361 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 397
 DB 358 CRSVRTKQMOVPLTSKGRSKSSSYSSSTTVKTSY 394
 RESULT 15
 ADO28601
 ID ADO28601 standard; protein; 389 AA.
 AC ADO28601;
 XX 12-AUG-2004 (first entry)
 DT 12-AUG-2004 (first entry)
 XX Human PAR2 protein SEQ ID NO:30.
 DE Human PAR2 protein SEQ ID NO:30.
 XX high-grade dysplasia; KGD; oesophageal adenocarcinoma;
 KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
 XX PAR2; chromosome 5.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Misc-difference 44
 FT /note="encoded by ACATCC"
 FT Misc-difference 101
 FT /note="encoded by CGAAGT"
 FT Misc-difference 158
 FT /note="encoded by TGTTC"
 FT Misc-difference 215
 FT /note="encoded by CCGGCC"
 FT Misc-difference 272
 FT /note="encoded by AACTCA"
 FT Misc-difference 329
 FT /note="encoded by CTTAAG"
 FT Misc-difference 386
 FT /note="encoded by GTTAAG"
 XX MO2004044178-A2.
 XX 27-MAY-2004.


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XX 13-NOV-2003; 2003WO-US036260.
PF
XX
XX 13-NOV-2002; 2002US-0425813P.
PR
XX
XX (GETH ) GENENTECH INC.
XX
XX Smith V;
PI
XX MPI; 2004-420319/39.
DR N-PSDB; ADO28600.
XX
XX Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the gene.
XX
XX Disclosure; SEQ ID NO 30; 256pp; English.
XX
XX The present invention describes a method for detecting high-grade
CC dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
CC (1) identifying an oesophageal tissue susceptible to oesophageal
CC adenocarcinoma; (2) determining the predilection of a mammalian tissue
CC to a neo-plastic transformation by detecting HGD in cells of the tissue;
CC and (3) detecting cancer in a patient. The method can be used in
CC detecting HGD and cancer in cells of a mammalian tissue sample. The
CC methods and compositions of the present invention can be used in treating
CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC represents human PAR2, which is used in the exemplification of the
CC present invention. The human PAR2 gene is located on chromosome 5.
XX
XX
SQ Sequence 389 AA;
Query Match 92.8%; Score 1884.5; DB 8; Length 389;
Best Local Similarity 97.0%; Pred. No. 1.3e-195;
Matches 384; Conservative 0; Mismatches 5; Indels 7; Gaps 7;
QY 2 RSPSAAMLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDGTSHTYKGVTVETVFSV 61
DB 1 RSPSAAMLGAAILLAASISCSGTIOGTNRSSKGRSLIGKVDG-SHTYKGVTVETVFSV 59
QY 62 DEFSASVLAGKLTTPFLPIYVTIVFAVGLPNGMALWFLFRTKQKPAVIYMANLALAD 121
DB 60 DEFSASVLAGKLTTPFLPIYVTIVFAVGLPNGMALWFLF-TKQKPAVIYMANLALAD 118
QY 122 LLSVTFPLKIAVHIGNNWYIGBALCNVLIGFFYGMNCSIIPTCLSVQRYWVIVNPM 181
DB 119 LLSVTFPLKIAVHIGNNWYIGBALCNVLIGFFYGMNCSIIPTCLSVQRYWVIVNPM 177
QY 182 GHSRKKANAIAGISLAIWLTLLVTIPLVYVKOTIFIPALNITTCDDVLPQOLLVGDMPN 241
DB 178 GHSRKKANAIAGISLAIWLTLLVTIPLVYVKOTIFIPALNITTCDDVLPQOLLVGDMPN 236
QY 242 YPLSLAIGVFLPAPFLTASAYVLMIRMSAMDENSEKRRKRAIKLIVTLGNYLICFT 301
DB 237 YPLSLAIGVFLPAPFLTASAYVLMIRMSAMDENSEKRRKRAIKLIVTLGNYLICFT 295
QY 302 PSNLLVVRHFFLIKSOGSHVYALYVALCLSTLNSCIDPPVTYFVSHDFRDAKNAALC 361
DB 296 PSNLLVVRHFFLIKSOGSHVYALYVALCLSTLNSCIDPPVTYFVSHDFRDAKNAALC 354
QY 362 RSVRTVKOMQVPLTSKHSRKSSTSSSTTVKTSY 397
DB 355 RSVRTVKOMQVPLTSKHSRKSSTSSSTTVKTSY 389
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